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LOGINID:sssept189dxw

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

***** Welcome to STN International *****

NEWS	1		Web Page for STN Seminar Schedule - N. America
NEWS	2	JAN 02	STN pricing information for 2008 now available
NEWS	3	JAN 16	CAS patent coverage enhanced to include exemplified prophetic substances
NEWS	4	JAN 28	USPATFULL, USPAT2, and USPATOLD enhanced with new custom IPC display formats
NEWS	5	JAN 28	MARPAT searching enhanced
NEWS	6	JAN 28	USGENE now provides USPTO sequence data within 3 days of publication
NEWS	7	JAN 28	TOXCENTER enhanced with reloaded MEDLINE segment
NEWS	8	JAN 28	MEDLINE and LMEEDLINE reloaded with enhancements
NEWS	9	FEB 08	STN Express, Version 8.3, now available
NEWS	10	FEB 20	PCI now available as a replacement to DPCI
NEWS	11	FEB 25	IFIREF reloaded with enhancements
NEWS	12	FEB 25	IMSPRODUCT reloaded with enhancements
NEWS	13	FEB 29	WPINDEX/WPIDS/WPIX enhanced with ECLA and current U.S. National Patent Classification
NEWS	14	MAR 31	IFICDB, IFIPAT, and IFIUDB enhanced with new custom IPC display formats
NEWS	15	MAR 31	CAS REGISTRY enhanced with additional experimental spectra
NEWS	16	MAR 31	CA/CAPLUS and CASREACT patent number format for U.S. applications updated
NEWS	17	MAR 31	LPCI now available as a replacement to LDPCI
NEWS	18	MAR 31	EMBASE, EMBAL, and LEMBASE reloaded with enhancements
NEWS	19	APR 04	STN AnaVist, Version 1, to be discontinued
NEWS	20	APR 15	WPIDS, WPINDEX, and WPIX enhanced with new predefined hit display formats
NEWS	21	APR 28	EMBASE Controlled Term thesaurus enhanced
NEWS	22	APR 28	IMSRSEARCH reloaded with enhancements
NEWS	23	MAY 30	INPAFAMDB now available on STN for patent family searching
NEWS	24	MAY 30	DGENE, PCTGEN, and USGENE enhanced with new homology sequence search option
NEWS	25	JUN 06	EPFULL enhanced with 260,000 English abstracts
NEWS	26	JUN 06	KOREAPAT updated with 41,000 documents
NEWS	27	JUN 13	USPATFULL and USPAT2 updated with 11-character patent numbers for U.S. applications
NEWS	28	JUN 19	CAS REGISTRY includes selected substances from web-based collections
NEWS	29	JUN 25	CA/CAPLUS and USPAT databases updated with IPC reclassification data
NEWS	30	JUN 30	AEROSPACE enhanced with more than 1 million U.S. patent records
NEWS	31	JUN 30	EMBASE, EMBAL, and LEMBASE updated with additional options to display authors and affiliated

organizations
 NEWS 32 JUN 30 STN on the Web enhanced with new STN AnaVist
 Assistant and BLAST plug-in
 NEWS 33 JUN 30 STN AnaVist enhanced with database content from EFFULL
 NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
 AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.
 NEWS HOURS STN Operating Hours Plus Help Desk Availability
 NEWS LOGIN Welcome Banner and News Items
 NEWS IPC8 For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that
 specific topic.

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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 13:55:21 ON 07 JUL 2008

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
 COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
 AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
 CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
 DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:55:47 ON 07 JUL 2008

69 FILES IN THE FILE LIST IN STINDEX

Enter SET DETAIL ON to see search term postings or to view
 search error messages that display as 0* with SET DETAIL OFF.

=> s Lactobacillus reuteri and toxin(p)bind? and CD4+ cell? and (food or tablet or
 dietary supplement or confectionery or drug)
 0* FILE ADISCTI

=> s Lactobacillus reuteri and toxin(p)bind? and CD4+ cells
 0* FILE ADISCTI

=> s Lactobacillus reuteri and toxin(p)bind?

0* FILE ADISNEWS
 0* FILE ANTE
 0* FILE AQUALINE
 0* FILE BIOENG
 1* FILE BIOTECHABS
 1* FILE BIOTECHDS
 0* FILE BIOTECHNO
 2 FILE CAPLUS
 0* FILE CEABA-VTB
 0* FILE CIN

27 FILES SEARCHED...

0* FILE ESBIOBASE
 0* FILE FOMAD

```

0* FILE FOREGE
2* FILE FROSTI
0* FILE FSTA
5 FILE GENBANK
1 FILE IFIPAT
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
1* FILE PASCAL
0* FILE PHARMAML
1 FILE SCISEARCH
1 FILE TOXCENTER
60 FILES SEARCHED...
21 FILE USPATFULL
3 FILE USPAT2
0* FILE WATER
2 FILE WPIDS
2 FILE WPINDEX

```

13 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STINDEX

L1 QUE LACTOBACILLUS REUTERI AND TOXIN(P) BIND?

=> file biotechds biotechabs caplus frosti genbank ifipat pascal scisearch
toxcenter uspatfull uspat2

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	3.90	4.11

FILE 'BIOTECHDS' ENTERED AT 13:59:37 ON 07 JUL 2008
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FILE 'BIOTECHABS' ACCESS NOT AUTHORIZED

FILE 'CAPLUS' ENTERED AT 13:59:37 ON 07 JUL 2008
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FILE 'GENBANK' ENTERED AT 13:59:37 ON 07 JUL 2008

FILE 'IFIPAT' ENTERED AT 13:59:37 ON 07 JUL 2008
COPYRIGHT (C) 2008 IFI CLAIMS(R) Patent Services (IFI)

FILE 'PASCAL' ENTERED AT 13:59:37 ON 07 JUL 2008
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FILE 'SCISEARCH' ENTERED AT 13:59:37 ON 07 JUL 2008
Copyright (c) 2008 The Thomson Corporation

FILE 'TOXCENTER' ENTERED AT 13:59:37 ON 07 JUL 2008
COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPATFULL' ENTERED AT 13:59:37 ON 07 JUL 2008
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPAT2' ENTERED AT 13:59:37 ON 07 JUL 2008
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

```
=> s l1
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
L2          38 L1
```

```
=> rem dup l2
DUP IS NOT VALID HERE
The DELETE command is used to remove various items stored by the
system.
```

To delete a saved query, saved answer set, saved L-number list, SDI request, batch request, mailing list, or user-defined cluster, format, or search field, enter the name. The name may include ? for left, right, or simultaneous left and right truncation.

Examples:

```
DELETE BIO?/Q          - delete query names starting with BIO
DELETE ?DRUG/A         - delete answer set names ending with DRUG
DELETE ?ELEC?/L        - delete L-number lists containing ELEC
DELETE ANTICOAG/S      - delete SDI request
DELETE ENZYME/B        - delete batch request
DELETE .MYCLUSTER      - delete user-defined cluster
DELETE .MYFORMAT       - delete user-defined display format
DELETE .MYFIELD        - delete user-defined search field
DELETE NAMELIST MYLIST - delete mailing list
```

To delete an ordered document or an offline print, enter its number.

Examples:

```
DELETE P123001C        - delete print request
DELETE D134002C        - delete document order request
```

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

```
DELETE L21             - delete a single L-number
DELETE L3-L6           - delete a range of L-numbers
DELETE LAST 4          - delete the last 4 L-numbers
DELETE L33-            - delete L33 and any higher L-number
DELETE -L55            - delete L55 and any lower L-number
DELETE L2-L6 RENUMBER  - delete a range of L-numbers and
                        renumber remaining L-numbers
DELETE RENUMBER        - renumber L-numbers after deletion of
                        intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

```
DELETE SAVED/Q - delete all saved queries
DELETE SAVED/A - delete all saved answer sets
DELETE SAVED/L - delete all saved L-number lists
DELETE SAVED - delete all saved queries, answer sets,
                and L-number lists
DELETE SAVED/S - delete all SDI requests
DELETE SAVED/B - delete all batch requests
DELETE CLUSTER - delete all user-defined clusters
DELETE FORMAT - delete all user-defined display formats
DELETE FIELD - delete all user-defined search fields
DELETE SELECT - delete all E-numbers
DELETE HISTORY - delete all L-numbers and restart the
                session at L1
```

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l2
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L2
L3          34 DUP REM L2 (4 DUPLICATES REMOVED)
```

```
=> s l3 and (tablet or food or dietary supplement or confectionery or drug) and
product
L4          27 L3 AND (TABLET OR FOOD OR DIETARY SUPPLEMENT OR CONFECTIONERY
                OR DRUG) AND PRODUCT
```

```
=> rem dup l4
DUP IS NOT VALID HERE
The DELETE command is used to remove various items stored by the
system.
```

To delete a saved query, saved answer set, saved L-number list, SDI request, batch request, mailing list, or user-defined cluster, format, or search field, enter the name. The name may include ? for left, right, or simultaneous left and right truncation.

Examples:

```
DELETE BIO?/Q - delete query names starting with BIO
DELETE ?DRUG/A - delete answer set names ending with DRUG
DELETE ?ELEC?/L - delete L-number lists containing ELEC
DELETE ANTICOAG/S - delete SDI request
DELETE ENZYME/B - delete batch request
DELETE .MYCLUSTER - delete user-defined cluster
DELETE .MYFORMAT - delete user-defined display format
DELETE .MYFIELD - delete user-defined search field
DELETE NAMELIST MYLIST - delete mailing list
```

To delete an ordered document or an offline print, enter its number.

Examples:

```
DELETE P123001C - delete print request
DELETE D134002C - delete document order request
```

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

```
DELETE L21           - delete a single L-number
DELETE L3-L6         - delete a range of L-numbers
DELETE LAST 4        - delete the last 4 L-numbers
DELETE L33-          - delete L33 and any higher L-number
DELETE -L55          - delete L55 and any lower L-number
DELETE L2-L6 RENUMBER - delete a range of L-numbers and
                      renumber remaining L-numbers
DELETE RENUMBER       - renumber L-numbers after deletion of
                      intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

```
DELETE SAVED/Q - delete all saved queries
DELETE SAVED/A - delete all saved answer sets
DELETE SAVED/L - delete all saved L-number lists
DELETE SAVED   - delete all saved queries, answer sets,
                  and L-number lists
DELETE SAVED/S - delete all SDI requests
DELETE SAVED/B - delete all batch requests
DELETE CLUSTER - delete all user-defined clusters
DELETE FORMAT  - delete all user-defined display formats
DELETE FIELD   - delete all user-defined search fields
DELETE SELECT  - delete all E-numbers
DELETE HISTORY - delete all L-numbers and restart the
                  session at L1
```

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l4
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L4
L5          27 DUP REM L4 (0 DUPLICATES REMOVED)
```

```
=> d l5 1-27
```

```
L5  ANSWER 1 OF 27  USPATFULL on SIN
AN  2007:296111  USPATFULL
TI  Lactobacillus acidophilus nucleic acid sequences encoding cell surface
    protein homologues and uses therefore
IN  Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
    Altermann, Eric, Palmerston North, NEW ZEALAND
    Buck, B. Logan, Banner Elk, NC, UNITED STATES
    Russell, W. Michael, Newburgh, IN, UNITED STATES
PA  North Carolina State University, Raleigh, NC, UNITED STATES (U.S.
    corporation)
PI  US 20070258955      A1  20071108
AI  US 2007-701335      A1  20070201 (11)
RLI  Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING
```

PRAI US 2003-465621P 20030425 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 5104
 INCL INCLM: 424/093.400
 INCLS: 435/252.100; 435/252.900; 435/320.100; 435/006.000; 435/007.100;
 435/070.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100
 NCL NCLM: 424/093.400
 NCLS: 435/006.000; 435/007.100; 435/070.100; 435/252.100; 435/252.900;
 435/320.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100
 IC IPCI A61K0035-00 [I,A]; A61K0038-00 [I,A]; A61P0001-00 [I,A];
 C07H0021-02 [I,A]; C07H0021-00 [I,C*]; C07K0016-00 [I,A];
 C07K0004-00 [I,A]; C12N0001-20 [I,A]; C12N0015-00 [I,A];
 C12P0021-04 [I,A]; C12Q0001-68 [I,A]
 IPCR A61K0035-00 [I,C]; A61K0038-00 [I,A]; A61K0038-00 [I,C];
 A61K0038-00 [I,A]; A61P0001-00 [I,C]; A61P0001-00 [I,A];
 C07H0021-00 [I,C]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
 C07K0004-00 [I,C]; C07K0004-00 [I,A]; C07K0014-195 [I,C*];
 C07K0014-335 [I,A]; C07K0016-00 [I,C]; C07K0016-00 [I,A];
 C12N0001-20 [I,C]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
 C12N0015-00 [I,C]; C12N0015-00 [I,A]; C12P0021-04 [I,C];
 C12P0021-04 [I,A]; C12P0021-06 [I,C*]; C12P0021-06 [I,A];
 C12Q0001-68 [I,C]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 2 OF 27 USPATFULL on SIN
 AN 2007:197155 USPATFULL
 TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface
 protein homologues and uses therefore
 IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
 Altermann, Eric, Palmerston North, NEW ZEALAND
 Buck, B. Logan, Banner Elk, NC, UNITED STATES
 Russell, W. Michael, Newburgh, IN, UNITED STATES
 PA North Carolina State University, Raleigh, NC, UNITED STATES, 27695-8210
 (U.S. corporation)
 PI US 20070172495 A1 20070726
 AI US 2007-701319 A1 20070201 (11)
 RLI Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING
 PRAI US 2003-465621P 20030425 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 5104
 INCL INCLM: 424/234.100
 INCLS: 514/044.000; 435/006.000; 435/007.320; 435/069.100; 435/252.900;
 435/471.000; 530/350.000; 536/023.700
 NCL NCLM: 424/234.100
 NCLS: 435/006.000; 435/007.320; 435/069.100; 435/252.900; 435/471.000;
 514/044.000; 530/350.000; 536/023.700
 IC IPCI A61K0048-00 [I,A]; A61K0039-02 [I,A]; C12Q0001-68 [I,A];
 G01N0033-554 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*];
 C12P0021-06 [I,A]; C07K0014-335 [I,A]; C07K0014-195 [I,C*]
 IPCR A61K0048-00 [I,C]; A61K0048-00 [I,A]; A61K0039-02 [I,C];
 A61K0039-02 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];
 C07K0014-195 [I,C]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
 C12P0021-06 [I,C]; C12P0021-06 [I,A]; C12Q0001-68 [I,C];
 C12Q0001-68 [I,A]; G01N0033-554 [I,C]; G01N0033-554 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 3 OF 27 USPATFULL on SIN
 AN 2007:140436 USPATFULL

TI Delivery of trefoil peptides
 IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
 Steidler, Lothar, Lokeren, BELGIUM
 Remaut, Erik Rene, Lovendegem, BELGIUM
 PI US 20070122427 A1 20070531
 AI US 2007-654879 A1 20070118 (11)
 RLI Division of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A 371
 of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000
 PRAI EP 1999-870143 19990705
 DT Utility
 FS APPLICATION
 LN.CNT 1335
 INCL INCLM: 424/200.100
 INCLS: 435/252.300; 435/252.900
 NCL NCLM: 424/200.100
 NCLS: 435/252.300; 435/252.900
 IC IPCI A61K0039-02 [I,A]; C12N0001-21 [I,A]
 IPCR A61K0039-02 [I,C]; A61K0039-02 [I,A]; C12N0001-21 [I,C];
 C12N0001-21 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 4 OF 27 USPATFULL on STN
 AN 2007:134502 USPATFULL
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
 (non-U.S. corporation)
 PI US 20070117183 A1 20070524
 AI US 2006-511140 A1 20060828 (11)
 RLI Division of Ser. No. US 2005-55822, filed on 11 Feb 2005, PENDING
 Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED
 PRAI DE 1999-19932125 19990709
 DE 1999-19932227 19990709
 DE 1999-19932228 19990709
 DE 1999-19932230 19990709
 DE 1999-19933005 19990714
 DE 1999-19933006 19990714
 DE 1999-19940764 19990827
 DE 1999-19940766 19990827
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 DE 1999-19942077 19990903
 DE 1999-19942079 19990903
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 DE 1999-19932126 19990709
 DE 1999-19932229 19990709
 DE 1999-19941396 19990831
 DE 1999-19942087 19990903
 DE 1999-19930476 19990701
 DE 1999-19931419 19990708
 DE 1999-19931420 19990708
 DE 1999-19932206 19990709
 DE 1999-19942088 19990903
 DE 1999-19942124 19990903
 DE 1999-19932928 19990714
 DE 1999-19931415 19990708
 DE 1999-19931424 19990708

DE 1999-19931428 19990708
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 DE 1999-19940765 19990827
 DE 1999-19941380 19990831
 DE 1999-19941394 19990831
 DE 1999-19942076 19990903
 DE 1999-19942086 19990903
 DE 1999-19942095 19990903
 DE 1999-19942129 19990903
 US 1999-141031P 19990625 (60)
 US 1999-142101P 19990702 (60)
 US 1999-148613P 19990812 (60)
 US 2000-187970P 20000309 (60)

DT Utility
 FS APPLICATION

LN.CNT 8386

INCL INCLM: 435/069.100
 INCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;
 536/023.200

NCL NCLM: 435/069.100
 NCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;
 536/023.200

IC IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12P0021-06 [I,A];
 C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
 C12N0009-10 [I,A]; C12N0015-74 [I,A]; C12N0001-21 [I,A]
 IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C];
 C12N0001-21 [I,A]; C12N0009-10 [I,C]; C12N0009-10 [I,A];
 C12N0015-74 [I,C]; C12N0015-74 [I,A]; C12P0013-00 [I,C];
 C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0021-06 [I,C];
 C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 5 OF 27 USPATFULL on SIN

AN 2007:127377 USPATFULL

TI Delivery of trefoil peptides

IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
 Steidler, Lother, Lokeren, BELGIUM
 Remaut, Erik Rene, Lovendegem, BELGIUM

PI US 20070110723 A1 20070517

AI US 2007-654985 A1 20070118 (11)

RLI Continuation of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A
 371 of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000

PRAI EP 1999-870143 19990705

DT Utility

FS APPLICATION
LN.CNT 1328
INCL INCLM: 424/093.200
INCLS: 424/093.450
NCL NCLM: 424/093.200
NCLS: 424/093.450
IC IPCI A61K0048-00 [I,A]
IPCR A61K0048-00 [I,C]; A61K0048-00 [I,A]; C12N0015-09 [I,C*];
C12N0015-09 [I,A]; A61K0035-66 [I,C*]; A61K0035-74 [I,A];
A61K0038-00 [I,C*]; A61K0038-00 [I,A]; A61P0001-00 [I,C*];
A61P0001-04 [I,A]; C07K0014-435 [I,C*]; C07K0014-575 [I,A];
C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0015-16 [I,C*];
C12N0015-16 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
C12R0001-01 [N,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 6 OF 27 USPATFULL on STN
AN 2007:130427 USPATFULL
TI Delivery of trefoil peptides
IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
Steidler, Lothar, Lokeren, BELGIUM
Remaut, Erik Rene, Lonendegem, BELGIUM
PA Vlaams Interuniversitair Instituut voor Biotechnologie, BELGIUM
(non-U.S. corporation)
PI US 7220418 B1 20070522
WO 2001002570 20010111
AI US 2000-30390 20000705 (10)
WO 2000-EP6343 20000705
20020416 PCT 371 date

PRAI EP 1999-870143 19990705
DT Utility
FS GRANTED
LN.CNT 1334
INCL INCLM: 424/200.100
INCLS: 424/093.450; 424/093.200; 424/234.100; 424/192.100; 514/925.000
NCL NCLM: 424/200.100
NCLS: 424/093.200; 424/093.450; 424/192.100; 424/234.100; 514/925.000
IC IPCI A01N0063-00 [I,A]; A61K0039-02 [I,A]; A61K0039-00 [I,A]
IPCR A01N0063-00 [I,C]; A01N0063-00 [I,A]; C12N0015-09 [I,C*];
C12N0015-09 [I,A]; A61K0035-66 [I,C*]; A61K0035-74 [I,A];
A61K0038-00 [I,C*]; A61K0038-00 [I,A]; A61K0039-00 [I,C];
A61K0039-00 [I,A]; A61K0039-02 [I,C]; A61K0039-02 [I,A];
A61K0048-00 [I,C*]; A61K0048-00 [I,A]; A61P0001-00 [I,C*];
A61P0001-04 [I,A]; C07K0014-435 [I,C*]; C07K0014-575 [I,A];
C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0015-16 [I,C*];
C12N0015-16 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
C12R0001-01 [N,A]
EXF 424/200.1; 424/192.1; 424/184.1; 424/234.1; 424/244.1; 424/246.1;
424/93.2; 424/93.45; 514/2; 514/925; 435/69.3; 435/69.1; 435/71.1;
435/252.9

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 7 OF 27 IFIPAT COPYRIGHT 2008 IFI on STN
AN 11053905 IFIPAT;IFIUDB;IFICDB
TI METHOD OF IMPROVING IMMUNE FUNCTION IN MAMALS USING LACTOBACILLUS
REUTERI STRAINS
IN Kang Ho-Jin (KR); Kwon Ik-boon (KR); Lee Dong-Seog (KR); Mollstam Bo (SE)
PA Unassigned Or Assigned To Individual (68000)
PI US 2006002907 A1 20060105
AI US 2002-531651 20021018
WO 2002-SE1903 20021018
20050415 PCT 371 date

20050415 PCT 102(e) date
 FI US 2006002907 20060105
 DT Utility; Patent Application - First Publication
 FS CHEMICAL
 APPLICATION
 ED Entered STN: 9 Jan 2006
 Last Updated on STN: 9 Jan 2006
 CLMN 9
 GI 1 Figure(s).

FIG. 1. Confirmation of inhibitory ability against the binding of vero cytotoxin(VT) and Gb3 receptor in a culture supernatant of *L. reuteri* through competitive ELISA. Each reacted as follows, on plates coated with Gb3, followed by performing ELISA using mAb against VT.

L5 ANSWER 8 OF 27 USPATFULL on STN
 AN 2006:274450 USPATFULL
 TI Gene products differentially expressed in cancerous cells
 IN Scott, Elizabeth M., Emeryville, CA, UNITED STATES
 Lamson, George, Emeryville, CA, UNITED STATES
 Kassam, Altaf, Emeryville, CA, UNITED STATES
 Zhang, Guozhong, Emeryville, CA, UNITED STATES
 Sakamoto, Doreen, Emeryville, CA, UNITED STATES
 Garcia, Pablo Dominguez, Emeryville, CA, UNITED STATES
 May, Theresa, Emeryville, CA, UNITED STATES
 Kennedy, Giulia C., Emeryville, CA, UNITED STATES
 Kang, Sanmao, Emeryville, CA, UNITED STATES
 Reinhard, Christoph, Emeryville, CA, UNITED STATES
 Jefferson, Ann Bennett, Emeryville, CA, UNITED STATES
 PA Chiron Corporation (U.S. corporation)
 PI US 20060234246 A1 20061019
 AI US 2004-934842 A1 20040902 (10)
 RLI Continuation-in-part of Ser. No. US 2002-165835, filed on 6 Jun 2002,
 ABANDONED Continuation of Ser. No. US 2000-490818, filed on 25 Jan 2000,
 GRANTED, Pat. No. US 6429302 Continuation-in-part of Ser. No. US
 2001-883152, filed on 15 Jun 2001, ABANDONED Continuation-in-part of
 Ser. No. WO 2003-US15465, filed on 16 May 2003, PENDING
 PRAI US 1999-118302P 19990202 (60)
 US 2000-211835P 20000615 (60)
 US 2003-445222P 20030204 (60)
 US 2002-381533P 20020517 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 17024
 INCL INCLM: 435/006.000
 INCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
 530/388.800; 536/023.500
 NCL NCLM: 435/006.000
 NCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
 530/388.800; 536/023.500
 IC IPCI C12Q0001-68 [I,A]; G01N0033-574 [I,A]; C07H0021-04 [I,A];
 C07H0021-00 [I,C*]; C12P0021-06 [I,A]; C07K0014-82 [I,A];
 C07K0016-30 [I,A]; C07K0016-18 [I,C*]
 IPCR C12Q0001-68 [I,C]; C12Q0001-68 [I,A]; C07H0021-00 [I,C];
 C07H0021-04 [I,A]; C07K0014-82 [I,C]; C07K0014-82 [I,A];
 C07K0016-18 [I,C]; C07K0016-30 [I,A]; C12P0021-06 [I,C];
 C12P0021-06 [I,A]; G01N0033-574 [I,C]; G01N0033-574 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 9 OF 27 USPATFULL on STN
 AN 2006:98984 USPATFULL
 TI *Corynebacterium glutamicum* genes encoding metabolic pathway proteins
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF

Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schröder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
(non-U.S. corporation)
PI US 20060084152 A1 20060420
AI US 2005-239674 A1 20050928 (11)
RLI Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED
Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23
Jun 2000, ABANDONED
PRAI DE 1999-19932125 19990709
DE 1999-19932227 19990709
DE 1999-19932228 19990709
DE 1999-19932230 19990709
DE 1999-19933005 19990714
DE 1999-19933006 19990714
DE 1999-19940764 19990827
DE 1999-19940766 19990827
DE 1999-19940832 19990827
DE 1999-19941378 19990831
DE 1999-19941379 19990831
DE 1999-19942077 19990903
DE 1999-19942079 19990903
DE 1999-19931418 19990708
DE 1999-19932126 19990709
DE 1999-19932229 19990709
DE 1999-19941396 19990831
DE 1999-19942087 19990903
DE 1999-19930476 19990701
DE 1999-19931419 19990708
DE 1999-19931420 19990708
DE 1999-19932206 19990709
DE 1999-19942088 19990903
DE 1999-19942124 19990903
DE 1999-19932928 19990714
DE 1999-19931415 19990708
DE 1999-19931424 19990708
DE 1999-19931428 19990708
DE 1999-19931434 19990708
DE 1999-19931435 19990708
DE 1999-19931443 19990708
DE 1999-19931453 19990708
DE 1999-19931457 19990708
DE 1999-19931465 19990708
DE 1999-19931478 19990708
DE 1999-19931510 19990708
DE 1999-19931541 19990708
DE 1999-19931573 19990708
DE 1999-19931592 19990708
DE 1999-19931632 19990708
DE 1999-19931634 19990708
DE 1999-19931636 19990708
DE 1999-19932130 19990708
DE 1999-19932186 19990709
DE 1999-19932922 19990714
DE 1999-19932926 19990714
DE 1999-19933004 19990714
DE 1999-19940765 19990827
DE 1999-19941380 19990831
DE 1999-19941394 19990831

DE 1999-19942076 19990903
 DE 1999-19942086 19990903
 DE 1999-19942095 19990903
 DE 1999-19942129 19990903
 DE 1999-19932124 19990709
 DE 1999-19932127 19990709
 DE 1999-19932133 19990709
 DE 1999-19932207 19990709
 DE 1999-19932208 19990709
 DE 1999-19932225 19990709
 DE 1999-19932914 19990709
 DE 1999-19940768 19990827
 DE 1999-19940831 19990827
 DE 1999-19941385 19990831
 US 1999-141031P 19990625 (60)
 US 1999-142101P 19990702 (60)
 US 1999-148613P 19990812 (60)
 US 2000-187970P 20000309 (60)
 US 1999-141031P 19990625 (60)
 US 1999-143694P 19990714 (60)
 US 1999-151778P 19990831 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 14822
 INCL INCLM: 435/113.000
 INCLS: 435/115.000; 435/252.300
 NCL NCLM: 435/113.000
 NCLS: 435/115.000; 435/252.300
 IC IPCI C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
 C12N0001-20 [I,A]
 IPCR C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];
 C12N0001-20 [I,A]; C12P0013-08 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.
 L5 ANSWER 10 OF 27 USPATFULL ON STN
 AN 2006:211028 USPATFULL
 TI Nucleic acid sequences relating to *Bacteroides fragilis* for diagnostics
 and therapeutics
 IN Breton, Gary L., Marlboro, MA, UNITED STATES
 PA Oscient Pharmaceuticals Corporation, Waltham, MA, UNITED STATES (U.S.
 corporation)
 PI US 7090973 B1 20060815
 AI US 2000-540209 20000404 (9)
 PRAI US 1999-128705P 19990409 (60)
 DT Utility
 FS GRANTED
 LN.CNT 38850
 INCL INCLM: 435/006.000
 INCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330
 NCL NCLM: 435/006.000
 NCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330
 IC IPCI C12Q0001-68 [I,A]; C12P0019-34 [I,A]; C12P0019-00 [I,C*];
 C07H0021-02 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*]
 EXF 435/91.1; 435/91.2; 435/6; 435/320.1; 435/325; 435/352.3; 536/23.1;
 536/24.1; 536/23.7; 536/24.32; 536/24.3; 514/44
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.
 L5 ANSWER 11 OF 27 USPATFULL ON STN
 AN 2006:146715 USPATFULL
 TI Nucleic acid and amino acid sequences relating to *Staphylococcus*
epidermidis for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn, Framingham, MA, UNITED STATES

Bush, David, Somerville, MA, UNITED STATES

PA Wyeth, Madison, NJ, UNITED STATES (U.S. corporation)

PI US 7060458 B1 20060613

AI US 1999-450969 19991129 (9)

RLI Continuation-in-part of Ser. No. US 1998-134001, filed on 13 Aug 1998,
Pat. No. US 6380370, issued on 30 Apr 2002

PRAI US 1997-64964P 19971108 (60)
US 1997-55779P 19970814 (60)

DT Utility

FS GRANTED

LN.CNT 35708

INCL INCLM: 435/069.100
INCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320

NCL NCLM: 435/069.100
NCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320

IC IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C*]
IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C*];
C12N0001-21 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]

EXF 435/6; 435/91.2; 435/69.1; 536/22.1; 536/23.1; 536/24.3

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 12 OF 27 USPATFULL on STN

AN 2005:299042 USPATFULL

TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF

PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
(non-U.S. corporation)

PI US 20050260707 A1 20051124

AI US 2005-55822 A1 20050211 (11)

RLI Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED

PRAI DE 1999-19932125 19990709
DE 1999-19932227 19990709
DE 1999-19932228 19990709
DE 1999-19932230 19990709
DE 1999-19933005 19990714
DE 1999-19933006 19990714
DE 1999-19940764 19990827
DE 1999-19940766 19990827
DE 1999-19940832 19990827
DE 1999-19941378 19990831
DE 1999-19941379 19990831
DE 1999-19942077 19990903
DE 1999-19942079 19990903
DE 1999-19931418 19990708
DE 1999-19932126 19990709
DE 1999-19932229 19990709
DE 1999-19941396 19990831
DE 1999-19942087 19990903
DE 1999-19930476 19990701
DE 1999-19931419 19990708
DE 1999-19931420 19990708
DE 1999-19932206 19990709
DE 1999-19942088 19990903
DE 1999-19942124 19990903
DE 1999-19932928 19990714
DE 1999-19931415 19990708
DE 1999-19931424 19990708
DE 1999-19931428 19990708

DE 1999-19931434 19990708
 DE 1999-19931435 19990708
 DE 1999-19931443 19990708
 DE 1999-19931453 19990708
 DE 1999-19931457 19990708
 DE 1999-19931465 19990708
 DE 1999-19931478 19990708
 DE 1999-19931510 19990708
 DE 1999-109931541 19990708
 DE 1999-19931573 19990708
 DE 1999-19931592 19990708
 DE 1999-19931632 19990708
 DE 1999-19931634 19990708
 DE 1999-19931636 19990708
 DE 1999-19932130 19990708
 DE 1999-19932186 19990709
 DE 1999-19932922 19990714
 DE 1999-19932926 19990714
 DE 1999-19933004 19990714
 DE 1999-19940765 19990827
 DE 1999-19941380 19990831
 DE 1999-19941394 19990831
 DE 1999-19942076 19990903
 DE 1999-19942086 19990903
 DE 1999-19942095 19990903
 DE 1999-19942129 19990903
 US 1999-141031P 19990625 (60)
 US 1999-142101P 19990702 (60)
 US 1999-148613P 19990812 (60)
 US 2000-187970P 20000309 (60)

DT Utility
 FS APPLICATION

LN.CNT 8777

INCL INCLM: 435/069.100
 INCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200

NCL NCLM: 435/069.100
 NCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200

IC [7]
 ICM C12P021-06
 ICS C12P013-04; C07H021-04; C12N001-20; C12N015-74; C12N009-10
 IPCI C12P0021-06 [I,C*]; C12P0013-04 [I,C*]; C12P0013-00 [I,C*];
 C07H0021-04 [I,C*]; C07H0021-00 [I,C*]; C12N0001-20 [I,C*];
 C12N0015-74 [I,C*]; C12N0009-10 [I,C*]
 IPCR C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
 C07K0014-34 [I,A]; C12N0001-20 [I,C*]; C12N0001-20 [I,A];
 C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];
 C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
 C12P0013-00 [I,C*]; C12P0013-04 [I,A]; C12P0021-06 [I,C*];
 C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 13 OF 27 USPATFULL on STN

AN 2005:268092 USPATFULL

TI Modified bacterial surface layer proteins

IN Pouwels, Pieter Hendrik, Rijswijk, NETHERLANDS

Smit, Egbert, Sittard, NETHERLANDS

Tielen, Frans, Prinsenbeek, NETHERLANDS

PI US 20050233408 A1 20051020

AI US 2003-500307 A1 20021223 (10)

WO 2002-EP14749 20021223

20041122 PCT 371 date

PRAI EP 2001-310937 20011228

DT Utility
 FS APPLICATION
 LN.CNT 2664
 INCL INCLM: 435/034.000
 INCLS: 530/395.000; 435/252.300
 NCL NCLM: 435/034.000
 NCLS: 435/252.300; 530/395.000
 IC [7]
 ICM C12Q001-04
 ICS C12N001-21; C07K014-335
 IPCI C12Q0001-04 [ICM,7]; C12N0001-21 [ICS,7]; C07K014-335 [ICS,7];
 C07K0014-195 [ICS,7,C*]
 IPCR C12N0015-09 [I,C*]; C12N0015-09 [I,A]; A61K0039-02 [I,C*];
 A61K0039-02 [I,A]; A61P0031-00 [I,C*]; A61P0031-04 [I,A];
 C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-15 [I,C*];
 C12N0001-15 [I,A]; C12N0001-19 [I,C*]; C12N0001-19 [I,A];
 C12N0001-20 [I,C*]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12N0005-10 [I,C*]; C12N0005-10 [I,A];
 C12N0015-31 [I,C*]; C12N0015-31 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 14 OF 27 USPATFULL on STN
 AN 2005:220997 USPATFULL
 TI Corynebacterium glutamicum genes encoding proteins involved in
 homeostasis and adaptation
 IN Pompejus, Markus, Waldsee, GERMANY, FEDERAL REPUBLIC OF
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF,
 D-67056 (non-U.S. corporation)
 PI US 20050191732 A1 20050901
 AI US 2003-721922 A1 20031124 (10)
 RLI Continuation of Ser. No. US 2000-603124, filed on 23 Jun 2000, ABANDONED
 PRAI DE 1999-19931418 19990708
 DE 1999-19932124 19990709
 DE 1999-19932126 19990709
 DE 1999-19932127 19990709
 DE 1999-19932133 19990709
 DE 1999-19932207 19990709
 DE 1999-19932208 19990709
 DE 1999-19932225 19990709
 DE 1999-19932229 19990709
 DE 1999-19932914 19990709
 DE 1999-19933006 19990709
 DE 1999-19940765 19990827
 DE 1999-19940768 19990827
 DE 1999-19940831 19990827
 DE 1999-19940832 19990827
 DE 1999-19941385 19990831
 DE 1999-19941396 19990831
 DE 1999-19942087 19990903
 US 1999-141031P 19990625 (60)
 US 1999-143694P 19990714 (60)
 US 1999-151778P 19990831 (60)

DT Utility
 FS APPLICATION
 LN.CNT 6552
 INCL INCLM: 435/106.000
 INCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;
 536/023.200

NCL NCLM: 435/106.000
 NCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;
 536/023.200

IC [7]
 ICM C12Q001-68
 ICS C07H021-04; C12P013-04; C12N009-10; C12N001-21; C12N015-74
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C*]; C12N0009-10 [ICS,7];
 C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7]
 IPCR C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
 C07K0014-34 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
 C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];
 C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
 C12P0001-04 [I,C*]; C12P0001-04 [I,A]; C12P0013-00 [I,C*];
 C12P0013-04 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 15 OF 27 USPATFULL on STN
 AN 2005:158196 USPATFULL
 TI Nucleic acid and amino acid sequences relating to streptococcus
 pneumoniae for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn A., Framingham, MA, UNITED STATES
 Bush, David, Somerville, MA, UNITED STATES
 PI US 20050136404 A1 20050623
 AI US 2003-617320 A1 20030710 (10)
 RLI Division of Ser. No. US 1998-107433, filed on 30 Jun 1998, PENDING
 PRAI US 1997-51553P 19970702 (60)
 US 1998-85131P 19980512 (60)

DT Utility
 FS APPLICATION

LN.CNT 12957

INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700
 NCL NCLM: 435/006.000
 NCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700

IC [7]
 ICM C12Q001-68
 ICS C07H021-04; C12N001-21; C07K014-315
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12N0001-21 [ICS,7]; C07K0014-315 [ICS,7]; C07K0014-195
 [ICS,7,C*]
 IPCR C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
 C07K0014-195 [I,C*]; C07K0014-315 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 16 OF 27 USPATFULL on STN
 AN 2005:131152 USPATFULL
 TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface
 protein homologues and uses therefore
 IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
 Alterman, Eric, Apex, NC, UNITED STATES
 Buck, B. Logan, Banner Elk, NC, UNITED STATES
 Russell, W. Michael, Newburg, IN, UNITED STATES
 PI US 20050112612 A1 20050526
 US 7348420 B2 20080325
 AI US 2004-831070 A1 20040423 (10)
 PRAI US 2003-465621P 20030425 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 6100
 INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 530/350.000;

536/023.200
 NCL NCLM: 536/023.100; 435/006.000
 NCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 530/350.000;
 536/023.200
 IC [7]
 ICM C12Q001-68
 ICS C07H021-04; C12P021-06; C12N009-00; C12N001-21; C07K014-335
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12P0021-06 [ICS,7]; C12N0009-00 [ICS,7]; C12N0001-21 [ICS,7];
 C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
 IPCI-2 C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12N0001-20 [I,A];
 C12N0015-00 [I,A]; C12P0001-20 [I,A]
 IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
 C07K0014-335 [I,A]; C12N0001-20 [I,C]; C12N0001-20 [I,A];
 C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0009-00 [I,C*];
 C12N0009-00 [I,A]; C12N0015-00 [I,C]; C12N0015-00 [I,A];
 C12P0021-06 [I,C*]; C12P0021-06 [I,A]; C12Q0001-68 [I,C*];
 C12Q0001-68 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 17 OF 27 USPATFULL on STN
 AN 2004:95339 USPATFULL
 TI Nutritional formulations containing synbiotic substances
 IN Kaup, Susan M., Collingswood, NJ, UNITED STATES
 Wilson, Jeffrey L., Doylestown, PA, UNITED STATES
 Kostek, Beverley M., Glen Mills, PA, UNITED STATES
 Frantz, David C., Pottstown, PA, UNITED STATES
 PA Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)
 PI US 20040072794 A1 20040415
 AI US 2003-681658 A1 20031008 (10)
 PRAI US 2002-418109P 20021011 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 542
 INCL INCLM: 514/054.000
 INCLS: 424/093.450
 NCL NCLM: 514/054.000
 NCLS: 424/093.450
 IC [7]
 ICM A61K045-00
 ICS A61K031-715
 IPCI A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]
 IPCR A23L0001-052 [I,C*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C*];
 A23L0001-29 [I,A]; A23L0001-30 [I,C*]; A23L0001-30 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 18 OF 27 USPATFULL on STN
 AN 2004:12970 USPATFULL
 TI Polynucleotides, materials incorporating them, and methods for using
 them
 IN Glenn, Matthew, Whenuapai, NEW ZEALAND
 Havukkala, Ilkka J., Remuera, NEW ZEALAND
 Lubbers, Mark, Palmerston North, NEW ZEALAND
 Dekker, James, Palmerston North, NEW ZEALAND
 PA GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND
 (non-U.S. corporation)
 PI US 20040009490 A1 20040115
 US 7125698 B2 20061024
 AI US 2002-264213 A1 20021003 (10)
 RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,
 PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug
 2000, GRANTED, Pat. No. US 6544772

PRAI US 1999-147853P 19990809 (60)
 US 1999-147852P 19990809 (60)
 US 1999-152032P 19990901 (60)
 US 1999-152031P 19990901 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 5375
 INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200
 NCL NCLM: 435/193.000; 435/006.000
 NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;
 435/252.300; 435/320.100; 536/023.200
 IC [7]
 ICM C12Q001-68
 ICS C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];
 C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
 IPCI-2 C12N0009-10 [I,A]
 IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C*];
 A23C0019-032 [I,A]; A61K0038-00 [N,C*]; A61K0038-00 [N,A];
 C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 19 OF 27 USPATFULL on STN
 AN 2004:250212 USPATFULL
 TI Nucleic acid and amino acid sequences relating to Streptococcus
 pneumoniae for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn A., Framingham, MA, United States
 Bush, David, Somerville, MA, United States
 PA Genome Therapeutics Corporation, Waltham, MA, United States (U.S.
 corporation)
 PI US 6800744 B1 20041005
 AI US 1998-107433 19980630 (9)
 PRAI US 1998-85131P 19980512 (60)
 US 1997-51553P 19970702 (60)
 DT Utility
 FS GRANTED
 LN.CNT 11545
 INCL INCLM: 536/023.100
 INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;
 536/024.100; 536/023.400; 536/024.320
 NCL NCLM: 536/023.100
 NCLS: 435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;
 536/024.100; 536/024.320
 IC [7]
 ICM C12Q001-68
 ICS C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;
 C07H021-04
 IPCI C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];
 C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
 IPCR C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
 C07K0014-195 [I,C*]; C07K0014-315 [I,A]
 EXF 536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;
 435/6
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 20 OF 27 USPATFULL on STN
 AN 2003:71519 USPATFULL
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF
Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF
Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF

PI US 20030049804 A1 20030313
AI US 2000-746660 A1 20001222 (9)

RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
2000, PENDING

PRAI DE 1999-19931420 19990708
US 1999-141031P 19990625 (60)
US 1999-142101P 19990702 (60)
US 1999-148613P 19990812 (60)
US 2000-187970P 20000309 (60)

DT Utility
FS APPLICATION

LN.CNT 15004

INCL INCLM: 435/115.000
INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200

NCL NCLM: 435/115.000
NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200

IC [7]
ICM C12P013-08
ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21
IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
C07H0023-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];
C12N0001-21 [ICS,7]
IPCR C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];
C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];
C12N0009-90 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 21 OF 27 USPATFULL on STN
AN 2003:95966 USPATFULL

TI Polynucleotides, materials incorporating them, and methods for using
them

IN Glenn, Matthew, Auckland, NEW ZEALAND
Havukkala, Ilkka J., Auckland, NEW ZEALAND
Blokberg, Leonard N., Auckland, NEW ZEALAND
Lubbers, Mark W., Palmerston North, NEW ZEALAND
Dekker, James, Palmerston North, NEW ZEALAND
Christensson, Anna C., Lund, SWEDEN
Holland, Ross, Palmerston North, NEW ZEALAND
O'Toole, Paul W., Palmerston North, NEW ZEALAND
Reid, Julian R., Palmerston North, NEW ZEALAND
Coolbear, Timothy, Palmerston North, NEW ZEALAND

PA Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.
corporation)
Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.
corporation)

PI US 6544772 B1 20030408
AI US 2000-634238 20000808 (9)

DT Utility
FS GRANTED

LN.CNT 2015

INCL INCLM: 435/252.300
INCLS: 435/320.100; 536/023.700

NCL NCLM: 435/252.300
 NCLS: 435/320.100; 536/023.700
 IC [7]
 ICM C12N001-21
 ICS C12N015-63; C12N015-31
 IPCI C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]
 IPCR A23C0019-00 [I,C*]; A23C0019-032 [I,A]; C07K0014-195 [I,C*];
 C07K0014-335 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
 C12N0015-31 [I,C*]; C12N0015-31 [I,A]
 EXF 435/252.3; 435/320.1; 536/23.7
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 22 OF 27 BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS on STN
 AN 1999-00562 BIOTECHDS
 TI Use of lactic and propionic acid bacteria;
 to bind mycotoxin to prevent their absorption or to purify
 contaminated food or feedstuff
 AU El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J
 PA Roy.Melbourne-Inst.Technol.
 LO Melbourne, Victoria, Australia.
 PI WO 9834503 13 Aug 1998
 AI WO 1998-AU63 6 Feb 1998
 PRAI AU 1997-5005 7 Feb 1997
 DT Patent
 LA English
 OS WPI: 1998-557001 [49]

L5 ANSWER 23 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): CP000705 GenBank (R)
 GenBank ACC. NO. (GBN): CP000705 AAOV01000000 AAOV01000001-AAOV01000097
 GenBank VERSION (VER): CP000705.1 GI:148530277
 SEQUENCE LENGTH (SQL): 1999618
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 17 Oct 2007
 DEFINITION (DEF): Lactobacillus reuteri F275,
 complete genome.
 SOURCE:
 ORGANISM (ORGN): Lactobacillus reuteri F275
 Lactobacillus reuteri F275
 Bacteria; Firmicutes; Lactobacillales;
 Lactobacillaceae; Lactobacillus
 PROJECT (PJID): GenomeProject:15766
 COMMENT:

URL -- <http://www.jgi.doe.gov>
 JGI Project ID: 4000135
 Source DNA available from Gerald Tannock
 (gerald.tannock@stonebow.otago.ac.nz)
 Bacteria available from DSMZ: DSM 20016
 Contacts: Gerald Tannock (gerald.tannock@stonebow.otago.ac.nz)
 Paul Richardson (microbes@cuba.jgi-psf.org)
 Quality assurance done by JGI-Stanford
 Annotation done by JGI-ORNL and JGI-PGF
 Finishing done by JGI-PGF
 Finished microbial genomes have been curated to close all gaps with
 greater than 98% coverage of at least two independent clones. Each
 base pair has a minimum q (quality) value of 30 and the total error
 rate is less than one per 50000.
 The JGI and collaborators endorse the principles for the
 distribution and use of large scale sequencing data adopted by the
 larger genome sequencing community and urge users of this data to
 follow them. It is our intention to publish the work of this

project in a timely fashion and we welcome collaborative
interaction on the project and analysis.
(<http://www.genome.gov/page.cfm?pageID=10506376>).

REFERENCE: 1 (bases 1 to 1999618)
AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.
TITLE (TI): Complete sequence of chromosome of
Lactobacillus reuteri DSM 20016
JOURNAL (SO): Unpublished
REFERENCE: 2 (bases 1 to 1999618)
AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (17-MAY-2007) US DOE Joint Genome Institute,
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698,
USA

FEATURES (FEAT):	Location	Qualifier
Feature Key		
source	1..1999618	/organism="Lactobacillus reuteri F275" /mol-type="genomic DNA" /strain="DSM 20016" /db-xref="taxon:299033" /note="F275 = DSM 20016 = JCM 1112"

L5 ANSWER 24 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM270397 GenBank (R)
GenBank ACC. NO. (GBN): AM270397
GenBank VERSION (VER): AM270397.1 GI:134084136
CAS REGISTRY NO. (RN): 928607-03-8
SEQUENCE LENGTH (SQL): 163680
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Plants, fungi, algae
DATE (DATE): 24 Mar 2007
DEFINITION (DEF): Aspergillus niger contig An18c0040, complete genome.
SOURCE: Aspergillus niger
ORGANISM (ORGN): Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic
Trichocomaceae; Aspergillus
REFERENCE: 1 (bases 150631 to 153085)
AUTHOR (AU): Habison,A.; Kubicek,C.P.; Rohr,M.
TITLE (TI): Partial purification and regulatory properties of
phosphofructokinase from Aspergillus niger
JOURNAL (SO): Biochem. J., 209 (3), 669-676 (1983)
OTHER SOURCE (OS): CA 99:171737
REFERENCE: 2 (bases 71863 to 73356)
AUTHOR (AU): Manney,T.R.
TITLE (TI): Expression of the BAR1 gene in Saccharomyces
cerevisiae: induction by the alpha mating pheromone of
an activity associated with a secreted protein

JOURNAL (SO): J. Bacteriol., 155 (1), 291-301 (1983)
 OTHER SOURCE (OS): CA 99:102121
 REFERENCE: 3 (bases 71863 to 73356)
 AUTHOR (AU): Jones, E.W.
 TITLE (TI): The synthesis and function of proteases in
 Saccharomyces: genetic approaches
 JOURNAL (SO): Annu. Rev. Genet., 18, 233-270 (1984)
 OTHER SOURCE (OS): CA 102:92538
 REFERENCE: 4 (bases 144032 to 145578)
 AUTHOR (AU): Brandsch, R.; Bichler, V.
 TITLE (TI): In vivo and in vitro expression of the
 6-hydroxy-D-nicotine oxidase gene of *Arthrobacter*
oxidans, cloned into *Escherichia coli*, as an
 enzymatically active, covalently flavinylated
 polypeptide
 JOURNAL (SO): FEBS Lett., 192 (2), 204-208 (1985)
 OTHER SOURCE (OS): CA 104:29597
 REFERENCE: 5 (bases 150631 to 153085)
 AUTHOR (AU): Schreier, G.; Kubicek, C.P.; Rohr, M.
 TITLE (TI): Inhibition of citric acid accumulation by manganese
 ions in *Aspergillus niger* mutants with reduced citrate
 control of phosphofructokinase
 JOURNAL (SO): J. Bacteriol., 165 (3), 1019-1022 (1986)
 OTHER SOURCE (OS): CA 104:165023
 REFERENCE: 6 (bases 156827 to 158638)
 AUTHOR (AU): Whittington, H.A.; Grant, S.; Roberts, C.F.; Lamb, H.;
 Hawkins, A.R.
 TITLE (TI): Identification and isolation of a putative permease
 gene in the quinic acid utilization (QUT) gene cluster
 of *Aspergillus nidulans*
 JOURNAL (SO): Curr. Genet., 12 (2), 135-139 (1987)
 OTHER SOURCE (OS): CA 107:91128
 REFERENCE: 7 (bases 54105 to 55762)
 AUTHOR (AU): Chisholm, V.T.; Lea, H.Z.; Rai, R.; Cooper, T.G.
 TITLE (TI): Regulation of allantoin transport in wild-type and
 mutant strains of *Saccharomyces cerevisiae*
 JOURNAL (SO): J. Bacteriol., 169 (4), 1684-1690 (1987)
 OTHER SOURCE (OS): CA 106:172689
 REFERENCE: 8 (bases 71863 to 73356)
 AUTHOR (AU): MacKay, V.L.; Welch, S.K.; Insley, M.Y.; Manney, T.R.;
 Holly, J.; Saari, G.C.; Parker, M.L.
 TITLE (TI): The *Saccharomyces cerevisiae* BAR1 gene encodes an
 exported protein with homology to pepsin
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 85 (1), 55-59 (1988)
 OTHER SOURCE (OS): CA 108:125658
 REFERENCE: 9 (bases 54105 to 55762)
 AUTHOR (AU): Rai, R.; Genbauffe, F.S.; Cooper, T.G.
 TITLE (TI): Structure and transcription of the allantoin permease
 gene (DAL5) from *Saccharomyces cerevisiae*
 JOURNAL (SO): J. Bacteriol., 170 (1), 266-271 (1988)
 OTHER SOURCE (OS): CA 109:17930
 REFERENCE: 10
 AUTHOR (AU): Hawkins, A.R.; Lamb, H.K.; Smith, M.; Keyte, J.W.;
 Roberts, C.F.
 TITLE (TI): Molecular organisation of the quinic acid utilization
 (QUT) gene cluster in *Aspergillus nidulans*
 JOURNAL (SO): Mol. Gen. Genet., 214 (2), 224-231 (1988)
 OTHER SOURCE (OS): CA 111:188522
 REFERENCE: 11 (bases 68231 to 69040)
 AUTHOR (AU): Honjo, M.; Nakayama, A.; Fukazawa, K.; Kawamura, K.;
 Ando, K.; Furutani, Y.
 TITLE (TI): A novel *Bacillus subtilis* gene involved in negative

control of sporulation and degradative-enzyme production
J. Bacteriol., 172 (4), 1783-1790 (1990)

JOURNAL (SO): CA 113:146166
OTHER SOURCE (OS):
REFERENCE: 12 (bases 5212 to 7379)

AUTHOR (AU): Nikawa, J.; Hosaka, K.; Tsukagoshi, Y.; Yamashita, S.
TITLE (TI): Primary structure of the yeast choline transport gene and regulation of its expression

JOURNAL (SO): J. Biol. Chem., 265 (26), 15996-16003 (1990)
OTHER SOURCE (OS): CA 114:18549
REFERENCE: 13 (bases 159975 to 161849)

AUTHOR (AU): Fling, M.E.; Kopf, J.; Tamarkin, A.; Gorman, J.A.; Smith, H.A.; Koltin, Y.
TITLE (TI): Analysis of a *Candida albicans* gene that encodes a novel mechanism for resistance to benomyl and methotrexate

JOURNAL (SO): Mol. Gen. Genet., 227 (2), 318-329 (1991)
OTHER SOURCE (OS): CA 116:100405
REFERENCE: 14 (bases 28874 to 30837)

AUTHOR (AU): Masuda, N.; Kitamura, N.; Saito, K.
TITLE (TI): Primary structure of protein moiety of *Penicillium notatum* phospholipase B deduced from the cDNA

JOURNAL (SO): Eur. J. Biochem., 202 (3), 783-787 (1991)
OTHER SOURCE (OS): CA 118:76020
REFERENCE: 15 (bases 100363 to 101496)

AUTHOR (AU): Sakoda, H.; Imanaka, T.
TITLE (TI): Cloning and sequencing of the gene coding for alcohol dehydrogenase of *Bacillus stearothermophilus* and rational shift of the optimum pH

JOURNAL (SO): J. Bacteriol., 174 (4), 1397-1402 (1992)
OTHER SOURCE (OS): CA 118:186708
REFERENCE: 16 (bases 20773 to 22555)

AUTHOR (AU): Kamoda, S.; Saburi, Y.
TITLE (TI): Structural and enzymatical comparison of lignostilbene- α , β -dioxxygenase isozymes, I, II, and III, from *Pseudomonas paucimobilis* TMY1009

JOURNAL (SO): Biosci. Biotechnol. Biochem., 57 (6), 931-934 (1993)
OTHER SOURCE (OS): CA 119:154577
REFERENCE: 17 (bases 80602 to 83154)

AUTHOR (AU): ElBerry, H.M.; Majumdar, M.L.; Cunningham, T.S.; Sumrada, R.A.; Cooper, T.G.
TITLE (TI): Regulation of the urea active transporter gene (*DUR3*) in *Saccharomyces cerevisiae*

JOURNAL (SO): J. Bacteriol., 175 (15), 4688-4698 (1993)
OTHER SOURCE (OS): CA 119:242524
REFERENCE: 18 (bases 23096 to 24052)

AUTHOR (AU): Roper, D.I.; Cooper, R.A.
TITLE (TI): Purification, nucleotide sequence and some properties of a bifunctional isomerase/decarboxylase from the homoprotocatechuate degradative pathway of *Escherichia coli* C

JOURNAL (SO): Eur. J. Biochem., 217 (2), 575-580 (1993)
OTHER SOURCE (OS): CA 119:265270
REFERENCE: 19 (bases 5212 to 7379)

AUTHOR (AU): Li, Z.; Brendel, M.
TITLE (TI): Co-regulation with genes of phospholipid biosynthesis of the CTR/HNMI-encoded choline/nitrogen mustard permease in *Saccharomyces cerevisiae*

JOURNAL (SO): Mol. Gen. Genet., 241 (5-6), 680-684 (1993)
OTHER SOURCE (OS): CA 121:28475
REFERENCE: 20 (bases 159975 to 161849)

AUTHOR (AU): Ben-Yaacov, R.; Knoller, S.; Caldwell, G.A.; Becker, J.M.;

Koltin, Y.

TITLE (TI): *Candida albicans* gene encoding resistance to benomyl and methotrexate is a multidrug resistance gene

JOURNAL (SO): *Antimicrob. Agents Chemother.*, 38 (4), 648-652 (1994)

OTHER SOURCE (OS): CA 121:2236

REFERENCE: 21 (bases 150631 to 153085)

AUTHOR (AU): Legisa, M.; Bencina, M.

TITLE (TI): Evidence for the activation of 6-phosphofructo-1-kinase by cAMP-dependent protein kinase in *Aspergillus niger*

JOURNAL (SO): *FEMS Microbiol. Lett.*, 118 (3), 327-333 (1994)

OTHER SOURCE (OS): CA 121:102759

REFERENCE: 22 (bases 138020 to 140061)

AUTHOR (AU): Kim, Y.J.; Bjorklund, S.; Li, Y.; Sayre, M.H.; Kornberg, R.D.

TITLE (TI): A multiprotein mediator of transcriptional activation and its interaction with the C-terminal repeat domain of RNA polymerase II

JOURNAL (SO): *Cell*, 77 (4), 599-608 (1994)

OTHER SOURCE (OS): CA 121:102149

REFERENCE: 23 (bases 38805 to 39836)

AUTHOR (AU): Downs, D.M.; Petersen, L.

TITLE (TI): *apbA*, a new genetic locus involved in thiamine biosynthesis in *Salmonella typhimurium*

JOURNAL (SO): *J. Bacteriol.*, 176 (16), 4858-4864 (1994)

OTHER SOURCE (OS): CA 121:197350

REFERENCE: 24 (bases 5212 to 7379)

AUTHOR (AU): Li, Z.; Brendel, M.

TITLE (TI): Sensitivity to nitrogen mustard in *Saccharomyces cerevisiae* is independently determined by regulated choline permease and DNA repair

JOURNAL (SO): *Mutat. Res.*, 315 (2), 139-145 (1994)

OTHER SOURCE (OS): CA 121:198201

REFERENCE: 25 (bases 85096 to 90863)

AUTHOR (AU): Szczypka, M.S.; Wemmie, J.A.; Moye-Rowley, W.S.; Thiele, D.J.

TITLE (TI): A yeast metal resistance protein similar to human cystic fibrosis transmembrane conductance regulator (CFTR) and multidrug resistance-associated protein

JOURNAL (SO): *J. Biol. Chem.*, 269 (36), 22853-22857 (1994)

OTHER SOURCE (OS): CA 122:26140

REFERENCE: 26 (bases 91484 to 93088)

AUTHOR (AU): Knight, S.A.; Tamai, K.T.; Kosman, D.J.; Thiele, D.J.

TITLE (TI): Identification and analysis of a *Saccharomyces cerevisiae* copper homeostasis gene encoding a homeodomain protein

JOURNAL (SO): *Mol. Cell. Biol.*, 14 (12), 7792-7804 (1994)

OTHER SOURCE (OS): CA 122:73697

REFERENCE: 27 (bases 85096 to 90863)

AUTHOR (AU): Wemmie, J.A.; Szczypka, M.S.; Thiele, D.J.; Moye-Rowley, W.S.

TITLE (TI): Cadmium tolerance mediated by the yeast AP-1 protein requires the presence of an ATP-binding cassette transporter-encoding gene, YCF1

JOURNAL (SO): *J. Biol. Chem.*, 269 (51), 32592-32597 (1994)

OTHER SOURCE (OS): CA 121:294343

REFERENCE: 28 (bases 20773 to 22555)

AUTHOR (AU): Kamoda, S.; Saburi, Y.

TITLE (TI): Cloning of a lignostilbene- α , β -dioxygenase isozyme gene from *Pseudomonas paucimobilis* TMY1009

JOURNAL (SO): *Biosci. Biotechnol. Biochem.*, 59 (10), 1866-1868 (1995)

OTHER SOURCE (OS): CA 124:47043

REFERENCE: 29 (bases 85096 to 90863)

AUTHOR (AU): Li, Z.S.; Szczypka, M.; Lu, Y.P.; Thiele, D.J.; Rea, P.A.
 TITLE (TI): The yeast cadmium factor protein (YCF1) is a vacuolar glutathione S-conjugate pump
 JOURNAL (SO): J. Biol. Chem., 271 (11), 6509-6517 (1996)
 OTHER SOURCE (OS): CA 124:226108
 REFERENCE: 30 (bases 33419 to 35477)
 AUTHOR (AU): Silva, J.C.; Minto, R.E.; Barry, C.E. III; Holland, K.A.; Townsend, C.A.
 TITLE (TI): Isolation and characterization of the versicolorin B synthase gene from *Aspergillus parasiticus*. Expansion of the aflatoxin B1 biosynthetic gene cluster
 JOURNAL (SO): J. Biol. Chem., 271 (23), 13600-13608 (1996)
 OTHER SOURCE (OS): CA 125:50401
 REFERENCE: 31 (bases 15614 to 17392)
 AUTHOR (AU): Covert, S.F.; Enkerli, J.; Miao, V.P.; VanEtten, H.D.
 TITLE (TI): A gene for maackiain detoxification from a dispensable chromosome of *Nectria haematococca*
 JOURNAL (SO): Mol. Gen. Genet., 251 (4), 397-406 (1996)
 OTHER SOURCE (OS): CA 125:106677
 REFERENCE: 32 (bases 131646 to 132375)
 AUTHOR (AU): Mitsuhashi, S.; Miyachi, S.
 TITLE (TI): Amino acid sequence homology between N- and C-terminal halves of a carbonic anhydrase in *Porphyridium purpureum*, as deduced from the cloned cDNA
 JOURNAL (SO): J. Biol. Chem., 271 (45), 28703-28709 (1996)
 OTHER SOURCE (OS): CA 125:321312
 REFERENCE: 33 (bases 85096 to 90863)
 AUTHOR (AU): Li, Z.S.; Lu, Y.P.; Zhen, R.G.; Szczypka, M.; Thiele, D.J.; Rea, P.A.
 TITLE (TI): A new pathway for vacuolar cadmium sequestration in *Saccharomyces cerevisiae*: YCF1-catalyzed transport of bis(glutathionato)cadmium
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 94 (1), 42-47 (1997)
 OTHER SOURCE (OS): CA 126:127966
 REFERENCE: 34 (bases 1241 to 3043)
 AUTHOR (AU): Saito, Y.; Ishii, Y.; Hayashi, H.; Imao, Y.; Akashi, T.; Yoshikawa, K.; Noguchi, Y.; Soeda, S.; Yoshida, M.; Niwa, M.; Hosoda, J.; Shimomura, K.
 TITLE (TI): Cloning of genes coding for L-sorbose and L-sorbose dehydrogenases from *Gluconobacter oxydans* and microbial production of 2-keto-L-gulonate, a precursor of L-ascorbic acid, in a recombinant *G. oxydans* strain
 JOURNAL (SO): Appl. Environ. Microbiol., 63 (2), 454-460 (1997)
 OTHER SOURCE (OS): CA 126:167180
 REFERENCE: 35 (bases 150631 to 153085)
 AUTHOR (AU): Ruijter, G.J.; Panneman, H.; Visser, J.
 TITLE (TI): Overexpression of phosphofructokinase and pyruvate kinase in citric acid-producing *Aspergillus niger*
 JOURNAL (SO): Biochim. Biophys. Acta, 1334 (2-3), 317-326 (1997)
 OTHER SOURCE (OS): CA 126:222695
 REFERENCE: 36 (bases 49850 to 51919)
 AUTHOR (AU): Prieto, R.; Woloshuk, C.P.
 TITLE (TI): *ord1*, an oxidoreductase gene responsible for conversion of O-methylsterigmatocystin to aflatoxin in *Aspergillus flavus*
 JOURNAL (SO): Appl. Environ. Microbiol., 63 (5), 1661-1666 (1997)
 OTHER SOURCE (OS): CA 127:13942
 REFERENCE: 37 (bases 17766 to 20491)
 AUTHOR (AU): Todd, R.B.; Murphy, R.L.; Martin, H.M.; Sharp, J.A.; Davis, M.A.; Katz, M.E.; Hynes, M.J.
 TITLE (TI): The acetate regulatory gene *facB* of *Aspergillus nidulans* encodes a Zn(II)2Cys6 transcriptional

activator
 JOURNAL (SO): Mol. Gen. Genet., 254 (5), 495-504 (1997)
 OTHER SOURCE (OS): CA 127:105007
 REFERENCE: 38 (bases 71863 to 73356)
 AUTHOR (AU): Ballensiefen, W.; Schmitt, H.D.
 TITLE (TI): Periplasmic Barl protease of *Saccharomyces cerevisiae* is active before reaching its extracellular destination
 JOURNAL (SO): Eur. J. Biochem., 247 (1), 142-147 (1997)
 OTHER SOURCE (OS): CA 127:187926
 REFERENCE: 39 (bases 52148 to 53720)
 AUTHOR (AU): Kuroyanagi, N.; Onogi, H.; Wakabayashi, T.; Hagiwara, M.
 TITLE (TI): Novel SR-protein-specific kinase, SRPK2, disassembles nuclear speckles
 JOURNAL (SO): Biochem. Biophys. Res. Commun., 242 (2), 357-364 (1998)
 OTHER SOURCE (OS): CA 128:241040
 REFERENCE: 40 (bases 113565 to 114733)
 AUTHOR (AU): MacDiarmid, C.W.; Gardner, R.C.
 TITLE (TI): Overexpression of the *Saccharomyces cerevisiae* magnesium transport system confers resistance to aluminum ion
 JOURNAL (SO): J. Biol. Chem., 273 (3), 1727-1732 (1998)
 OTHER SOURCE (OS): CA 128:177021
 REFERENCE: 41 (bases 135940 to 137166)
 AUTHOR (AU): Wang, H.Y.; Lin, W.; Dyck, J.A.; Yeakley, J.M.; Songyang, Z.; Cantley, L.C.; Fu, X.D.
 TITLE (TI): SRPK2: a differentially expressed SR protein-specific kinase involved in mediating the interaction and localization of pre-mRNA splicing factors in mammalian cells
 JOURNAL (SO): J. Cell Biol., 140 (4), 737-750 (1998)
 OTHER SOURCE (OS): CA 128:306636
 REFERENCE: 42 (bases 38805 to 39836)
 AUTHOR (AU): Frodyma, M.E.; Downs, D.
 TITLE (TI): ApbA, the ketopantoate reductase enzyme of *Salmonella typhimurium* is required for the synthesis of thiamine via the alternative pyrimidine biosynthetic pathway
 JOURNAL (SO): J. Biol. Chem., 273 (10), 5572-5576 (1998)
 OTHER SOURCE (OS): CA 128:305459
 REFERENCE: 43 (bases 106231 to 106803)
 AUTHOR (AU): Woloshuk, C.P.; Prieto, R.
 TITLE (TI): Genetic organization and function of the aflatoxin B1 biosynthetic genes
 JOURNAL (SO): FEMS Microbiol. Lett., 160 (2), 169-176 (1998)
 OTHER SOURCE (OS): CA 128:290649
 REFERENCE: 44 (bases 93571 to 94963)
 AUTHOR (AU): Philp, N.J.; Yoon, H.; Grollman, E.F.
 TITLE (TI): Monocarboxylate transporter MCT1 is located in the apical membrane and MCT3 in the basal membrane of rat RPE
 JOURNAL (SO): Am. J. Physiol., 274 (6 Pt 2), R1824-R1828 (1998)
 OTHER SOURCE (OS): CA 129:159493
 REFERENCE: 45 (bases 93571 to 94963)
 AUTHOR (AU): Wilson, M.C.; Jackson, V.N.; Heddle, C.; Price, N.T.; Pilegaard, H.; Juel, C.; Bonen, A.; Montgomery, I.; Hutter, O.F.; Halestrap, A.P.
 TITLE (TI): Lactic acid efflux from white skeletal muscle is catalyzed by the monocarboxylate transporter isoform MCT3
 JOURNAL (SO): J. Biol. Chem., 273 (26), 15920-15926 (1998)
 OTHER SOURCE (OS): CA 129:159801
 REFERENCE: 46 (bases 153410 to 154508)
 AUTHOR (AU): Dekkers, L.C.; van der Bij, A.J.; Mulders, I.H.;

Phoelich, C.C.; Wentwoord, R.A.; Glandorf, D.C.;
Wijffelman, C.A.; Lugtenberg, B.J.

TITLE (TI): Role of the O-antigen of lipopolysaccharide, and possible roles of growth rate and of NADH:ubiquinone oxidoreductase (nuo) in competitive tomato root-tip colonization by *Pseudomonas fluorescens* WCS365
Mol. Plant Microbe Interact., 11 (8), 763-771 (1998)

JOURNAL (SO): CA 129:200426
OTHER SOURCE (OS):

REFERENCE: 47 (bases 146433 to 148685)
AUTHOR (AU): Saito, K.; Yamazaki, H.; Ohnishi, Y.; Fujimoto, S.; Takahashi, E.; Horinouchi, S.

TITLE (TI): Production of trehalose synthase from a basidiomycete, *Grifola frondosa*, in *Escherichia coli*
Appl. Microbiol. Biotechnol., 50 (2), 193-198 (1998)

JOURNAL (SO): CA 130:956
OTHER SOURCE (OS):

REFERENCE: 48 (bases 122486 to 123895)
AUTHOR (AU): Kimura, M.; Matsumoto, G.; Shingu, Y.; Yoneyama, K.; Yamaguchi, I.

TITLE (TI): The mystery of the trichothecene 3-O-acetyltransferase gene. Analysis of the region around Tri101 and characterization of its homologue from *Fusarium sporotrichioides*
FEBS Lett., 435 (2-3), 163-168 (1998)

JOURNAL (SO): CA 130:11163
OTHER SOURCE (OS):

REFERENCE: 49 (bases 146433 to 148685)
AUTHOR (AU): Saito, K.; Kase, T.; Takahashi, E.; Horinouchi, S.

TITLE (TI): Purification and characterization of a trehalose synthase from the basidiomycete *grifola frondosa*
Appl. Environ. Microbiol., 64 (11), 4340-4345 (1998)

JOURNAL (SO): CA 130:34870
OTHER SOURCE (OS):

REFERENCE: 50 (bases 14029 to 15172)
AUTHOR (AU): Feng, Y.; Khoo, H.E.; Poh, C.L.

TITLE (TI): Purification and characterization of gentisate 1,2-dioxygenases from *Pseudomonas alcaligenes* NCIB 9867 and *Pseudomonas putida* NCIB 9869
Appl. Environ. Microbiol., 65 (3), 946-950 (1999)

JOURNAL (SO): CA 130:32223
OTHER SOURCE (OS):

REFERENCE: 51 (bases 59070 to 60560)
AUTHOR (AU): Bosch, R.; Moore, E.R.; Garcia-Valdes, E.; Pieper, D.H.

TITLE (TI): NahW, a novel, inducible salicylate hydroxylase involved in mineralization of naphthalene by *Pseudomonas stutzeri* AN10
J. Bacteriol., 181 (8), 2315-2322 (1999)

JOURNAL (SO): CA 131:70144
OTHER SOURCE (OS):

REFERENCE: 52
AUTHOR (AU): DeZwaan, T.M.; Carroll, A.M.; Valent, B.; Sweigard, J.A.

TITLE (TI): Magnaporthe grisea pth11p is a novel plasma membrane protein that mediates appressorium differentiation in response to inductive substrate cues
Plant Cell, 11 (10), 2013-2030 (1999)

JOURNAL (SO): CA 132:47358
OTHER SOURCE (OS):

REFERENCE: 53 (bases 122486 to 123895)
AUTHOR (AU): McCormick, S.P.; Alexander, N.J.; Trapp, S.E.; Hohn, T.M.

TITLE (TI): Disruption of Tri101, the gene encoding trichothecene 3-O-acetyltransferase, from *Fusarium sporotrichioides*
Appl. Environ. Microbiol., 65 (12), 5252-5256 (1999)

JOURNAL (SO): CA 132:118174
OTHER SOURCE (OS):

REFERENCE: 54 (bases 111907 to 113460)
AUTHOR (AU): Muraguchi, H.; Kamada, T.

TITLE (TI): A mutation in the *eln2* gene encoding a cytochrome P450 of *Coprinus cinereus* affects mushroom morphogenesis
Fungal Genet. Biol., 29 (1), 49-59 (2000)

JOURNAL (SO):

OTHER SOURCE (OS): CA 134:96073

REFERENCE: 55 (bases 108826 to 111209)

AUTHOR (AU): Yu, J.; Chang, P.K.; Bhatnagar, D.; Cleveland, T.E.

TITLE (TI): Genes encoding cytochrome P450 and monooxygenase enzymes define one end of the aflatoxin pathway gene cluster in *Aspergillus parasiticus*

JOURNAL (SO): Appl. Microbiol. Biotechnol., 53 (5), 583-590 (2000)

OTHER SOURCE (OS): CA 133:291807

REFERENCE: 56 (bases 122486 to 123895)

AUTHOR (AU): Muhitch, M.J.; McCormick, S.P.; Alexander, N.J.; Hohn, T.M.

TITLE (TI): Transgenic expression of the TR101 or PDR5 gene increases resistance of tobacco to the phytotoxic effects of the trichothecene 4,15-diacetoxyscirpenol

JOURNAL (SO): Plant Sci., 157 (2), 201-207 (2000)

OTHER SOURCE (OS): CA 133:306551

REFERENCE: 57 (bases 107279 to 108340)

AUTHOR (AU): Cheng, Q.; Thomas, S.M.; Kostichka, K.; Valentine, J.R.; Nagarajan, V.

TITLE (TI): Genetic analysis of a gene cluster for cyclohexanol oxidation in *Acinetobacter* sp. Strain SE19 by in vitro transposition

JOURNAL (SO): J. Bacteriol., 182 (17), 4744-4751 (2000)

OTHER SOURCE (OS): CA 134:37832

REFERENCE: 58 (bases 100363 to 101496)

AUTHOR (AU): Jorvall, H.; Hoog, J.O.; Persson, B.; Pares, X.

TITLE (TI): Pharmacogenetics of the alcohol dehydrogenase system

JOURNAL (SO): Pharmacology, 61 (3), 184-191 (2000)

OTHER SOURCE (OS): CA 134:38655

REFERENCE: 59

AUTHOR (AU): Calabrese, D.; Bille, J.; Sanglard, D.

TITLE (TI): A novel multidrug efflux transporter gene of the major facilitator superfamily from *Candida albicans* (FLU1) conferring resistance to fluconazole

JOURNAL (SO): Microbiology (Reading, Engl.), 146 (PT 11), 2743-2754 (2000)

OTHER SOURCE (OS): CA 135:1055

REFERENCE: 60

AUTHOR (AU): Deising, H.B.; Werner, S.; Wernitz, M.

TITLE (TI): The role of fungal appressoria in plant infection

JOURNAL (SO): Microbes Infect., 2 (13), 1631-1641 (2000)

REFERENCE: 61 (bases 43783 to 45994)

AUTHOR (AU): Smith, S.

TITLE (TI): The world according to PARP

JOURNAL (SO): Trends Biochem. Sci., 26 (3), 174-179 (2001)

OTHER SOURCE (OS): CA 135:15779

REFERENCE: 62 (bases 131646 to 132375)

AUTHOR (AU): Cronk, J.D.; Endrizzi, J.A.; Cronk, M.R.; O'Neill, J.W.; Zhang, K.Y.

TITLE (TI): Crystal structure of *E. coli* beta-carbonic anhydrase, an enzyme with an unusual pH-dependent activity

JOURNAL (SO): Protein Sci., 10 (5), 911-922 (2001)

REFERENCE: 63 (bases 43783 to 45994)

AUTHOR (AU): Ziegler, M.; Oei, S.L.

TITLE (TI): A cellular survival switch: poly(ADP-ribosylation) stimulates DNA repair and silences transcription

JOURNAL (SO): Bioessays, 23 (6), 543-548 (2001)

REFERENCE: 64 (bases 43783 to 45994)

AUTHOR (AU): Herceg, Z.; Wang, Z.Q.

TITLE (TI): Functions of poly(ADP-ribose) polymerase (PARP) in DNA repair, genomic integrity and cell death

JOURNAL (SO): Mutat. Res., 477 (1-2), 97-110 (2001)

OTHER SOURCE (OS): CA 136:145570

REFERENCE: 65 (bases 15614 to 17392)
 AUTHOR (AU): Mundodi, S.R.; Watson, B.S.; Lopez-Meyer, M.; Paiva, N.L.
 TITLE (TI): Functional expression and subcellular localization of the *Nectria haematococca* Makl phytoalexin detoxification enzyme in transgenic tobacco
 JOURNAL (SO): Plant Mol. Biol., 46 (4), 421-432 (2001)
 OTHER SOURCE (OS): CA 135:285870
 REFERENCE: 66 (bases 1 to 163680)
 AUTHOR (AU): Pel, H.J.; de Winde, J.H.; Archer, D.B.; Dyer, P.S.; Hofmann, G.; Schaap, P.J.; Turner, G.; de Vries, R.P.; Albarg, R.; Albermann, K.; Andersen, M.R.; Bendtsen, J.D.; Benen, J.A.; van den Berg, M.; Breestraat, S.; Caddick, M.X.; Contreras, R.; Cornell, M.; Coutinho, P.M.; Danchin, E.G.; Debets, A.J.; Dekker, P.; van Dijk, P.W.; van Dijk, A.; Dijkhuizen, L.; Driessen, A.J.; d'Enfert, C.; Geysens, S.; Goosen, C.; Groot, G.S.; de Groot, P.W.; Guillemette, T.; Henrissat, B.; Herweijer, M.; van den Hombergh, J.P.; van den Hondel, C.A.; van der Heijden, R.T.; van der Kaaij, R.M.; Klis, F.M.; Kools, H.J.; Kubicek, C.P.; van Kuyk, P.A.; Lauber, J.; Lu, X.; van der Maarel, M.J.; Meulenbergh, R.; Menke, H.; Mortimer, M.A.; Nielsen, J.; Oliver, S.G.; Olsthoorn, M.; Pal, K.; van Peij, N.N.; Ram, A.F.; Rinas, U.; Roubos, J.A.; Sagt, C.M.; Schmoll, M.; Sun, J.; Ussery, D.; Varga, J.; Verweken, W.; van de Vondervoort, P.J.; Wedler, H.; Wosten, H.A.; Zeng, A.P.; van Ooyen, A.J.; Visser, J.; Stam, H.
 TITLE (TI): Genome sequencing and analysis of the versatile cell factory *Aspergillus niger* CBS 513.88
 JOURNAL (SO): Nat. Biotechnol., 25 (2), 221-231 (2007)
 OTHER SOURCE (OS): CA 146:310276
 REFERENCE: 67 (bases 1 to 163680)
 AUTHOR (AU): Pel, H.J.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O. Box 1, 2600 MA Delft, THE NETHERLANDS

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intron	complement(6160..6224)	/locus-tag="An18g00960" /number=4
exon	complement(6225..6602)	/locus-tag="An18g00960" /number=5
intron	complement(6603..6673)	/locus-tag="An18g00960" /number=5
exon	complement(6674..6746)	/locus-tag="An18g00960"

intron	complement(6747..6799)	/number=6 /locus-tag="An18g00960"
exon	complement(6800..6899)	/number=6 /locus-tag="An18g00960"
intron	complement(6900..7248)	/number=7 /locus-tag="An18g00960"
exon	complement(7249..7379)	/number=7 /locus-tag="An18g00960"
gene	complement(<7770..>8415)	/number=8 /locus-tag="An18g00970"
mRNA	complement(join(<7770..8282,8380..>8415))	/locus-tag="An18g00970"
CDS	complement(join(7770..8282,8380..8415))	/locus-tag="An18g00970"

/note="unnamed protein product;
 Title: weak similarity to
 hypothetical protein BAA96207.1 -
Oryza sativa"
 /codon-start=1
 /protein-id="CAK47174.1"
 /db-xref="GI:134084141"
 /translation="MLCTHAGGEGARSGRPDDRQ
 GHQPI\$VALWL\$CAPPPGFLSGRTS
 LASAGISNPDGATAVNTCETV\$GLTACGQDCL
 SSRAALAE\$LL\$GLCCV\$GGG\$GRA\$F
 PANPNKMDRY\$LL\$LYCRLGLTLDGPIVVVVVHTLS
 LSCSPPTQLHPPPL\$ASLH\$SFFPP
 ESLGRVPISIIYAHMRHAAAKIV"
 /locus-tag="An18g00970"
 /number=1

exon	complement(7770..8282)	/locus-tag="An18g00970"
intron	complement(8283..8379)	/number=1
exon	complement(8380..8415)	/locus-tag="An18g00970"
gene	<8621..>9700	/number=2 /locus-tag="An18g00980"
mRNA	join(<8621..8764,8830..9156,9214..9356,9406..>9700)	/locus-tag="An18g00980"
CDS	join(8621..8764,8830..9156,9214..9356,9406..9700)	/locus-tag="An18g00980"

/note="unnamed protein product;
 Function: *M. grisea* Pth11 is a
 pathogenicity gene. Function: *M.*
grisea Pth11p is likely to be
 involved in host surface
 recognition. Function: *M. grisea*
 pth11 mutants of strain 4091-5-8
 are nonpathogenic due to a defect
 in appressorium differentiation.
 Localization: in *M. grisea*, a
 Pth11-green fluorescent protein
 fusion localised to the cell
 membrane and vacuoles. Similarity:
 similarity of the predicted *A.*
niger protein and *M. grisea* Pth11
 is limited to the N-terminal half
 of the protein sequences. Title:
 weak similarity to integral
 membrane protein PTH11 -
Magnaporthe grisea plasma

		membrane"
		/citation=[52]
		/codon-start=1
		/protein-id="CAK47175.1"
		/db-xref="GI:134084142"
		/translation="MTDHSAAVKVVTCTFLLVSF
		IADVACLTITNQVLRKRVSSVALL
		LSTLIASIASGAAVSVAATHGLQASPLTDAQVV
		VMQKALYSMEVLVYVLTGLGKLSV
		MVLFYLLSSTGQSKSVLAATGLLLIWMVVMVIV
		VCLQCHPPEVWNVIGGTCCLDLSGI
		WIAFGVMNVLVEIMIIAVPSFIIIFRLKLSLKRRL
		VVISCFGIRILDIAGSIVQLCYVR
		NFKIHADSMPMTNVWQWAICSQVLQTVAILSACV
		PYLREFLEFPSPGMFKPTLKHPT
		VQSAYNATKCSDSDIELMRPESTKDT"
sig-peptide	8621..8698	/locus-tag="An18g00980"
		/inference="protein
		motif:SignalP:2.0"
mat-peptide	join(8699..8764, 8830..9156,9214..9356, 9406..9697)	/locus-tag="An18g00980"
exon	8621..8764	/product="unnamed"
		/locus-tag="An18g00980"
		/number=1
intron	8765..8829	/locus-tag="An18g00980"
		/number=1
exon	8830..9156	/locus-tag="An18g00980"
		/number=2
intron	9157..9213	/locus-tag="An18g00980"
		/number=2
exon	9214..9356	/locus-tag="An18g00980"
		/number=3
intron	9357..9405	/locus-tag="An18g00980"
		/number=3
exon	9406..9700	/locus-tag="An18g00980"
		/number=4
gene	complement(<9787..>9927	/locus-tag="An18g00990"
)	
mRNA	complement(<9787..>9927	/locus-tag="An18g00990"
)	
CDS	complement(9787..9927)	/locus-tag="An18g00990"
		/note="unnamed protein product;
		Title: strong similarity to EST
		an-1359 -Aspergillus niger"
		/codon-start=1
		/protein-id="CAK47176.1"
		/db-xref="GI:134084143"
		/translation="MRAATLLVALSAVALALPT
		TNNVERAAADANVRQMDLTVAAI SK"
sig-peptide	complement(9877..9927)	/locus-tag="An18g00990"
		/inference="protein
		motif:SignalP:2.0"
mat-peptide	complement(9790..9876)	/locus-tag="An18g00990"
		/product="unnamed"
exon	complement(9787..9927)	/locus-tag="An18g00990"
		/number=1
gene	<10500..>11479	/locus-tag="An18g01000"
mRNA	join(<10500..10749, 10812..11041, 11105..>11479)	/locus-tag="An18g01000"
CDS	join(10500..10749,	/locus-tag="An18g01000"

10812..11041,
11105..11479)

exon 10500..10749
intron 10750..10811
exon 10812..11041
intron 11042..11104
exon 11105..11479
gene <11980..>13464
mRNA join(<11980..12137,
12198..>13464)
CDS join(11980..12137,
12198..13464)

/note="unnamed protein product;
Similarity: the nucleotide
sequence of the ORF shows strong
similarity to the ESTs an-2192 and
an-2204 of *A. niger*. Title: strong
similarity to EST an-2192
-*Aspergillus niger*"
/codon-start=1
/protein-id="CAK47177.1"
/db-xref="GI:134084144"
/translation="MYSYEKVNRRDDSDQGLLAE
DSERVAPQPRVSRFPSWTNALLL
GLLFSLSLNVGFVFKQGHNVPIQDLDPDAAMAK
QRSPTYTGLAWDTHKPYSHHSEYTS
ENATHADEMMEESLSMDPMVIAPTWEWAQSKGLSD
SWAFPWDSNRRYFIKVFHQLHCL
KLMRHSYHELWGGQESSIPAPHIEHCLDSLRLQDL
MCKADDTMPPSLQLLNGGEGEQQM
QCKDFDKLVAWSKAPERNACYKRLTDYKPIVHSI
ERYAFCPEDSEHYPTMSKYFEEHG HYADPFSE"
/locus-tag="An18g01000"
/number=1
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/number=2
/locus-tag="An18g01000"
/number=3
/locus-tag="An18g01010"
/locus-tag="An18g01010"
/locus-tag="An18g01010"
/inference="profile:COGS:COG0477"
/note="unnamed protein product;
Function: FLU1 of *C. albicans*
facilitates resistance to
fluconazole and cycloheximide in
the fluconazole-hypersensitive *S.*
cerevisiae strain YKKB-13 lacking
the ABC (ATP-binding cassette)
transporter gene PDR5. Function:
FLU1 of *C. albicans* facilitates
resistance to mycophenolic acid in
C. albicans. Function: FLU1 of *C.*
albicans is involved in the
resistance to azol derivatives in
C. albicans. Function: MDRL of *C.*
albicans facilitates resistance to
the anti-mitotic drug benomyl and
to the dihydrofolate reductase
inhibitor methotrexate.
Similarity: N-terminus of the *A.*
niger protein is app. 120 aa
shorter than in FLU1 of *C.*
albicans. Similarity: the
predicted *A. niger* protein shows
strong similarity to fluconazole

resistance protein FLU1 of *C. albicans*, which is a permease belonging to the major facilitator superfamily. Title: strong similarity to fluconazole resistance protein FLU1 - *Candida albicans*"

/citation=[59]
/codon-start=1
/protein-id="CAK47178.1"
/db-xref="GI:134084145"
/translation="MDEEDGHCKETEVTQSTSP
VDSADYDPFDPQTRSTTYKWITVV
LVAGLSTMVQLSTIIAAPVSPSILAHFHSNALLY
RTLIVSIWELGEIVAPLLWGPLE
LYGRQWPLNIANLFFVAFLAGTAASTSIQMLIAF
RFLSGAATAASAIGPGIVSDFPE
ESRGRAMSIMSLTGALGPVVGPIGVSYLGEKAGW
RWAFWLPTIATGTLSLLILVVYRE
TYSVTLQKRKARQQNPESGSKSPEDTDKTASQVF
FKAILRPLRLLIRSPMLILVTFYL
SVVYGYTYLVMTTIAPLFQDVYGFSEGAAGLAF
GLCLGLILGAFGLCSFLLDRYVRTA
RARSGETSKPEQRLPPVLIACFVMSGGLFLFGWTA
QYHVQWIAPIIGTGIIGFGLVSTT
ITLQTYVVDLFGIYAASATSAMLVPRNACAAFLP
LAGPPLFDRLGYNWGGTLLALIVL
VFSMLPLIFINYGERLRGKNLLDD"
/locus-tag="An18g01010"
/number=1
/locus-tag="An18g01010"
/number=1
/locus-tag="An18g01010"
/number=2
/locus-tag="An18g01020"
72)
complement(join(<14029..
14318,14411..14845,
14917..>15172))
/locus-tag="An18g01020"
complement(join(14029..
14318,14411..14845,
14917..15172))
/EC-number="1.13.11.4"
/inference="profile:COGS:COG3435"
/inference="similar to AA
sequence:UniProtKB:AF173167.3"
/note="unnamed protein product;
Complex: the estimated molecular
mass of the purified gentisate 1,
2-dioxygenase of *P. alcaligenes*
was 154 kDa, with a subunit mass
of 39 kDa. its structure is
deduced to be a tetramer. Remark:
gentisate 1,2-dioxygenase of *P.*
alcaligenes exhibits typical
saturation kinetics and has an
apparent Km of 92 microM for
gentisate. this enzyme has broad
substrate specificities towards
alkyl and halogenated gentisate
analogs. Similarity: the predicted
A. niger protein shows strong

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similarity to gentisate
1,2-dioxygenase of P. alcaligenes
and conserved hypothetical
proteins from other procaryotic
species. Title: strong similarity
to gentisate 1,2-dioxygenases xlnE
- Pseudomonas alcaligenes"
/citation=[50]
/codon-start=1
/protein-id="CAK47179.1"
/db-xref="GI:134084146"
/translation="MSPSACNTGSGADSAEQLL
QDLKKSNTLPLWTQMTRLNPPEFN
PTAVPFIWRYDSIRENLLRAGELVTEKQAERRVL
MLVNPARDAPYITDTLYAGLQLVM
PNETAPAHRRHTAFAMRYIIIEGNGGFTAVHGKRIK
MQKGDVILIPTWNYHDHGKDGTF
MIWLDGLDLNPNRHFVDFVHYDQPRYPADVD
SATSPIVFPWDMKKAELDKAPGIW
AVRRYLADGSEGGSAERVDAITSSLPQETTS
VYHVIAGSGCSEIGDKTLVWETGD
TFCVPSWYKYRHIAAEGETVYLYRFDDKPMISAL
GFYRSIDTDLATLVSQ"

exon      complement(14029..14318 /locus-tag="An18g01020"
)
intron    complement(14319..14410 /locus-tag="An18g01020"
)
exon      complement(14411..14845 /locus-tag="An18g01020"
)
intron    complement(14846..14916 /locus-tag="An18g01020"
)
exon      complement(14917..15172 /locus-tag="An18g01020"
)
gene      <15614..>17392 /number=3
mRNA      join(<15614..15661, /locus-tag="An18g01030"
15723..16281, /locus-tag="An18g01030"
16347..16503,
16584..16739,
16803..16942,
17034..>17392)
CDS       join(15614..15661, /locus-tag="An18g01030"
15723..16281,
16347..16503,
16584..16739,
16803..16942,
17034..17392)

/inference="profile:COGS:COG0654"
/inference="profile:PFAM:PF01360"
/note="unnamed protein product;
Function: MakI from N.
haematococca specifically
hydroxylates the phytoalexins
medicarpin and
maackiain, converting them to less
fungitoxic derivatives.
Localization: heterologous
expression of the MakI cDNA

```

construct in plants indicated that Mak1 protein accumulates in the plant cytoplasm, associated with endoplasmic reticulum membranes. Similarity: the predicted A. niger protein shows strong similarity to Mak1 from the fungal pathogen N. haematococca. Mak1 belongs to the flavin-containing mono-oxygenases. best matches are with putative salicylate hydroxylases of several procaryotic species. Title: strong similarity to maackiain detoxification protein 1 MAK1 - Nectria haematococca endoplasmatic reticulum"

/citation=[31]
/citation=[65]
/codon-start=1
/protein-id="CAK47180.1"
/db-xref="GI:134084147"
/translation="MASTRMSAQSTIADLRVPDY
PSNCLQFTQQLTASATHLPOKDA
SVRLNIILAGAGLGLATAIALAQAGHAVKIYEQ
TPVLGEVVGAGIQIPSNSTRILFSL
GLQSYLEPYVTAPESISFRWQNGKVI GLTKLIP
NFVNNFKAPYYVIHRADFHSALCQ
KALDVGEIELGAKVVVDYDPVGSITLADGKHS
ADLIVAADGIKSVARNVVLQGDDEM
RFQGPGEAAYRAVVDVGKMRDPDLWSWILEKPA
NIWIGDSRHVMTYTIGAGKAFNMV
LSHPMTDPGTWKPEALEDMKAEFGQWDPILSK
IIGMVEKTVKWPPLLGTGLLQNWTV
GKLVILGDAAHAMVPYMSQGAAMAVEDGIALSRS
LSHMTSRDQLQKALSIFQEVRRKR
AGHMQEASLLNGKLWHFFDGSLLQQARDEAMAPEV
QGIPFSHSPNQWSDPATQMWCYGY
DAEEAIDIAWMESLEARVDCVH"
/locus-tag="An18g01030"
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/number=5
/locus-tag="An18g01030"
/number=6
/locus-tag="An18g01040"
/locus-tag="An18g01040"

exon	15614..15661
intron	15662..15722
exon	15723..16281
intron	16282..16346
exon	16347..16503
intron	16504..16583
exon	16584..16739
intron	16740..16802
exon	16803..16942
intron	16943..17033
exon	17034..17392
gene	<17766..>20491
mRNA	join(<17766..17864,

CDS

17939..18039,
18108..18343,
18398..19163,
19373..19935,
20037..20252,
20325..>20491)
join(17766..17864,
17939..18039,
18108..18343,
18398..19163,
19373..19935,
20037..20252,
20325..20491)

/locus-tag="An18g01040"

/inference="profile:PFAM:PF00172"
/inference="similar to AA
sequence:UniProtKB:ENU56097.1"
/note="unnamed protein product;
Phenotype: facB recessive loss of
function mutants in *A. nidulans*
are deficient in acetate induction
of acetyl-CoA synthase, isocitrate
lyase, malate
synthase, acetamidase, and
NADP-isocitrate dehydrogenase.
Similarity: the predicted *A. niger*
protein shows similarity to
acetate regulatory DNA binding
protein FacB (facB) from *A.*
nidulans, which belongs to the
GAL4-type zinc cluster
transcriptional activators. Title:
similarity to acetate regulatory
DNA binding protein facB -
Aspergillus nidulans"
/citation={37}
/codon-start=1
/protein-id="CAK47181.1"
/db-xref="GI:134084148"
/translation="MDFAPELPTPQGQSVKRRRV
ALACDACRTRKSRCDGRRPKCGMC
EDLGFECAYTPSTTTNIIVQKDYLRDLEERVKS
LETSMATVKS DLSGFASQINGSMF
DAPRKENPLSNQSERFSDFAGTEDTIDAMGAVAF
ADEEDCGFFGPSSNIAFLRHLSCA
VAHSASAQKEITSPFLDRVAYDGGFVSATRPSSP
SHDQRPESLEGEKFDKFPPEE
SLALIHRYFADTGLLFPYIHPPTFFETAYELKDN
SKRVRRTWLGLLNIIAMAKLTAV
SGTTS AETGISEAIYYHRA LSLCKGEILRGTTL
EVGRYSIYAPVVRARVPVYLRTKI
NTVQYLLVMGQYLGQTKQSVQAWTIHGLAVKAAL
QLGLHSKGASRAFTLEQEVKRT
WFGCVVLDRVRANFLNRRKTIQQANIRVSTLYK
QIANI IDRIYGQNLGCDSPLSIGE
TVGRVLGIENQLFSWVLGLPESLRQVTQSMREE
IERSEVGDEGHHKLYPLKFRIILT
LRYFHVQILLHRPILVKFLDATGSPSGLEADEVKL
LNDIGYSSMNKCVDSAMGIIIDIIH
ELVSTTGWQKDLLGAWWYSLYYTFNAALVVIIGAM
WVQRNRDTS EDPVDNCGNNNNMDI
YLSRAVLTQLNLVGNRMVRCKYYLDQLITLLG
LQADRIAETGIISGMNPNVAGNST

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exon      17766..17864      TGFDFPSLGLIEGEGFMIDDDFFPGFARGSGFERW"
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                                     /number=1
intron    17865..17938      /locus-tag="An18g01040"
                                     /number=1
exon      17939..18039      /locus-tag="An18g01040"
                                     /number=2
intron    18040..18107      /locus-tag="An18g01040"
                                     /number=2
exon      18108..18343      /locus-tag="An18g01040"
                                     /number=3
intron    18344..18397      /locus-tag="An18g01040"
                                     /number=3
exon      18398..19163      /locus-tag="An18g01040"
                                     /number=4
intron    19164..19372      /locus-tag="An18g01040"
                                     /number=4
exon      19373..19935      /locus-tag="An18g01040"
                                     /number=5
intron    19936..20036      /locus-tag="An18g01040"
                                     /number=5
exon      20037..20252      /locus-tag="An18g01040"
                                     /number=6
intron    20253..20324      /locus-tag="An18g01040"
                                     /number=6
exon      20325..20491      /locus-tag="An18g01040"
                                     /number=7
gene      complement(<20773..>22555) /locus-tag="An18g01050"
mRNA      complement(join(<20773.. /locus-tag="An18g01050"
.21444,21501..21638,
21710..22119,
22180..22303,
22370..>22555))
CDS       complement(join(20773.. /locus-tag="An18g01050"
21444,21501..21638,
21710..22119,
22180..22303,
22370..22555))

/EC-number="1.13.11.43"
/inference="profile:COGS:COG3670"
/inference="profile:PFAM:PF03055"
/inference="similar to AA
sequence:PIR:JC4324"
/note="unnamed protein product;
Catalytic activity:
lignostilbene-alpha,beta-dioxygena
se isozymes (LSD-I, II, and III)
of P. paucimobilis catalyse the
reaction
1,2-bis(4-hydroxy-3-methoxyphenyl)
ethylene + O(2) = 2 vanillin
Cofactor:
lignostilbene-alpha,beta-dioxygena
se isozymes (LSD-I, II, and III)
of P. paucimobilis require iron as
a cofactor. Complex: LSD-I, II,
and III consist of alpha
alpha,alpha beta, and beta beta
subunits, respectively. they show
different specificities for
several substrates that are

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stilbene and styrene derivatives. Function: LSD of *P. paucimobilis* catalyses the oxidative cleavage of the interphenyl double bond in the synthetic substrate and lignin-derived stilbenes. it is responsible for the degradation of a diarylpropane-type structure in lignin. Similarity: the predicted *A. niger* protein shows strong similarity to subunit lsdB of lignostilbene-alpha,beta-dioxygenase isozyme LSD-III of *P. paucimobilis* and related dioxygenases from several plant species. Title: strong similarity to subunit lsdB of lignostilbene-alpha,beta-dioxygenase isozyme LSD-III -*Pseudomonas paucimobilis*"

/citation=[16]
/citation=[28]
/codon-start=1
/protein-id="CAK47182.1"
/db-xref="GI:134084149"
/translation="MTETRTTIAFPARPQFSGFMK
PCRVEGETLNLEVLGDLPTDIDGV
FYRVMPDPQLPFFIENDFWNGDGNITAFRFHDG
RVSFQQRYRTEKFVVRERQAQRAL
IAQLTLFLWSIEGKYRNKFTDAVEFKVRSTANTN
IVYFNGQLLALKEDSPPYAMDPT
LETGLYDFDGLPFSMTFTAHPKFDPETGEMICF
GYEARGDGTDPVCYYTVGPDGKFT
EVVNLVAPVVMIHDFAVTDNWVIFPIIPQLCDI
ERMKQGGEH*QWSPETPLYLGVIP
RRGAKTADVKWFQYKNSFFGHTANAHEDSSGNLI
IDLGLSEKNVFFWVWPDAGQNAPEP
SSIRSQLVRFTINPRAEDNLNTEPRILQADNSEF
YRIDDRYATKPHRHVFFDMMDPSL
GTDFAPIAPVLGGGYPLYNLARFDNVTGETEVY
FPGKTHMVQEPVFI PRSELAEEGD
GYLLALVNNYDSMSSELHLLDTADFTTRARAKILL
PVRLRPGLHGSHVDGSDVPLSAAR L"

exon	complement(20773..21444	/locus-tag="An18g01050"
)	
		/number=1
intron	complement(21445..21500	/locus-tag="An18g01050"
)	
		/number=1
exon	complement(21501..21638	/locus-tag="An18g01050"
)	
		/number=2
intron	complement(21639..21709	/locus-tag="An18g01050"
)	
		/number=2
exon	complement(21710..22119	/locus-tag="An18g01050"
)	
		/number=3
intron	complement(22120..22179	/locus-tag="An18g01050"
)	
		/number=3
exon	complement(22180..22303	/locus-tag="An18g01050"

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)
intron      complement(22304..22369) /number=4
                                                    /locus-tag="An18g01050"
)
exon        complement(22370..22555) /number=4
                                                    /locus-tag="An18g01050"
)
gene        <23096..>24052           /number=5
mRNA        join(<23096..23375,      /locus-tag="An18g01060"
                23443..23571,        /locus-tag="An18g01060"
                23667..>24052)
CDS         join(23096..23375,       /locus-tag="An18g01060"
                23443..23571,
                23667..24052)

                                                    /EC-number="5.3.3.10"
                                                    /inference="profile:COGS:COG0179"
                                                    /inference="profile:PFAM:PF01557"
                                                    /note="unnamed protein product;
Catalytic activity:
5-carboxymethyl-2-hydroxymuconate
delta-isomerase from E. coli
catalyses the reaction
5-carboxymethyl-2-hydroxymuconate
= 5-carboxy-2-oxohept-3-enedioate.
Pathway:
5-carboxymethyl-2-hydroxymuconate
delta-isomerase from E. coli is
involved in tyrosine and
phenylalanine metabolism.
Similarity: the predicted A. niger
protein shows strong similarity to
5-carboxymethyl-2-hydroxymuconate
delta-isomerase from E. coli and
many putative
2-hydroxyhepta-2,4-diene-1,
7-dioate isomerases from several
prokaryotic and eucaryotic
organisms. Title: strong
similarity to
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FPFPIFFKPNCTCVHDHGEFVVIPRIAQNDQADYE
VIGKDAKDVPVESALDYIAAYTVG
NDISSRKLQRPAYAGVVPQWGFSGFDTFAPLG
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CDS	join(24984..25058, 25166..25301, 25564..25745, 25812..26003, 26080..26144, 26206..26646, 26722..27303, 27423..27426)	/locus-tag="An18g01070"

/inference="profile:COGS:COG0477"
 /note="unnamed protein product;
 Function: FLU1 of C. albicans
 facilitates resistance to
 fluconazole and cycloheximide in
 the fluconazole-hypersensitive S.
 cerevisiae strain YKKB-13 lacking
 the ABC (ATP-binding cassette)
 transporter gene PDR5. Function:
 FLU1 of C. albicans facilitates
 resistance to mycophenolic acid in
 C. albicans. Function: FLU1 of C.
 albicans is involved in the
 resistance to azol derivatives in
 C. albicans. Function: MDR1 of C.
 albicans facilitates resistance to
 the anti-mitotic drug benomyl and
 to the dihydrofolate reductase
 inhibitor methotrexate.
 Similarity: N-terminus of the A.
 niger protein is app. 120 aa
 shorter than in FLU1 of C.
 albicans. Similarity: the
 predicted A. niger protein shows
 strong similarity to fluconazole
 resistance protein FLU1 of C.
 albicans, which is a permease
 belonging to the major facilitator
 superfamily. Title: similarity to
 fluconazole resistance protein
 FLU1 - Candida albicans"
 /citation=[59]
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 MGGAGLSVAVPVLMOOLORSOAEVLTLLTNFL

LGIGNIFWVPLAVKFGKRASIISS
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 ESIVPEIVADIFFVHERATMMAIY
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 ALASFNIIVLLVFLFPESTFKRPEP
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 NTPPFKGVLPRPFHYNKDASFFKAV
 ISPLKLLVHPSVCWGIIFYGISLSPQIIMIFNFS
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 GFLACYGGGYLSDIVNRMIAQRSSSSSIRPEQR
 LISLIPGMAIGPAGCILLAFACGH
 KLHWAIAVGFVGMVSFGTVYTPNIALTYIVHLHQ
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		/number=6
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intron	27304..27422	/locus-tag="An18g01070"
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mRNA	complement (join (<27797..28220,28259..28342,28450..28550,28602..>28667))	/locus-tag="An18g01080"
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 FYSLRFVVSHPHPTVPANHTVSGTNTSFDHRVI

sig-peptide	complement (join (28506..28550,28602..28667))	LVSNNSQWIIINPWSIGRTLSWPGP VKSLEAGRYGHLRKHNPAAEELNFASSNKHCC VMLRAYYYPRVQEEYLLRLFLYRC LKDTASFATVRKKDQSLNVHESLQSTYPGGIFRV AAKADFPAGEGSKSFRQTMCWALL LKYGVF"
		/locus-tag="An18g01080"
mat-peptide	complement (join (27800..28220,28259..28342,28450..28505))	/inference="protein motif:SignalP:2.0"
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exon	complement (27797..28220)	/product="hypothetical protein"
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intron	complement (28221..28258)	/number=1
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		/locus-tag="An18g01080"
intron	complement (28551..28601)	/number=3
		/locus-tag="An18g01080"
exon	complement (28602..28667)	/number=3
		/locus-tag="An18g01080"
gene mRNA	<28874..>30837 join (<28874..29683,29736..29875,29925..>30837)	/number=4
		/locus-tag="An18g01090"
CDS	join (28874..29683,29736..29875,29925..30837)	/locus-tag="An18g01090"
		/EC-number="3.1.1.5"
lysophospholipase catalyses the reaction 2-lysophosphatidylcholine + H(2)O = glycerophosphocholine + a fatty acid anion. Pathway: lysophospholipase is involved in phospholipid degradation. Similarity: the predicted A. niger protein shows strong similarity to the protein sequences lysophospholipase (sequence 5 and sequence 7) of patents WO0127251-A/5 and WO0127251-A/7 from A. oryzae (AC# AX112082 and AC# AX112084) and to other fungal lysophospholipases. Title: strong similarity to lysophospholipase from patent WO0127251-A -		

		Aspergillus oryzae extracellular/secretion proteins" /citation=[14] /codon-start=1 /protein-id="CAK47186.1" /db-xref="GI:134084153" /translation="MLSLLISAAAATLASALELP QGYSPPDPVSCPTNLSWIRPAVGLS RDEAQWVEGRKNVILGSLDAYLKRNLNLDLDDFTDE YISRLNNTSQTPIMGMAISGGGFG SAYITGTGLIRALDRLPAANEQRTGGLLQSMYTL SGLSGGSWPAVSFPFSYNFPTADEI VDYWKPEIDRFFFTVINTSAAEATGKAIFEQIATK YLAGFEVALSDYLGRGFAYEFIPG QSGGLNTTFSGIRNLSNFINHQMPPMIIHLASVE PEDAEYYDLLVPSSNGTIFDLTPF EFGAWDGDVHAFIPTEWLGNQLSNGIPVNQSKCW KGFDRSSLVIGTSADAFNFWYLES VSNGLTGQFAKRSTTHESSLTKRLSQPANLNALV DAFQETFDLNLITQISYSKFFNPFT NLSLSTGNTHKSSTLNLVDGSETGQTIPLWGQIQ PARNVDFIIAWDDSDQADDPYSWNN GTNLNYNTYLAANATGLFPFPIIPPSRTMMNLNYTL HPQFFGCDANLITTTGDDRAPILVLY MANAPYSAYTNFSEFWQTETSROQMGEIFVNSFDI VTQANGSWDGEWAECMGCAVERS LARVGMERTRQCQRCFERYCWDGTLDERDPGVLD PTLVLDPGVKFGLWATNPY" /locus-tag="An18g01090" /inference="protein motif:SignalP:2.0"
sig-peptide	28874..28921	
mat-peptide	join(28922..29683, 29736..29875, 29925..30834)	/locus-tag="An18g01090"
exon	28874..29683	/product="unnamed" /locus-tag="An18g01090" /number=1
intron	29684..29735	/locus-tag="An18g01090" /number=1
exon	29736..29875	/locus-tag="An18g01090" /number=2
intron	29876..29924	/locus-tag="An18g01090" /number=2
exon	29925..30837	/locus-tag="An18g01090" /number=3
gene	complement(<30960..>32218)	/locus-tag="An18g01100"
mRNA	complement(join(<30960.. .31045,31081..31220, 31273..31630, 31702..>32218))	/locus-tag="An18g01100"
CDS	complement(join(30960.. 31045,31081..31220, 31273..31630, 31702..32218))	/locus-tag="An18g01100"
		/EC-number="1.1.1.-" /inference="profile:COGS:COG0604" /inference="profile:COGS:COG1064" /inference="profile:PFAM:PF00107" /note="unnamed protein product; Remark: the patent does not provide further information about

the function of the protein.
 Similarity: the predicted A. niger protein shows strong similarity to the protein sequence alcohol dehydrogenase (sequence 19) of patent EP0845532-A/19 from an unclassified organism (AC# A92108) and to other zinc-containing dehydrogenases. Title: strong similarity to alcohol dehydrogenase from patent EP0845532-A - Unclassified organism cytoplasm"
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 EVIAVGEKVKTLAVGDRRAAPITDT
 EQITERATKRSWLAADEDGVMADYIVYDESVLCK
 LPAYLDWVQASMI PCAGVTAWSA
 L KGMRIQOTVLVQGTGGVSMFALKALAAGLRVVL
 TSSSDAKLOAIKEKYAGSAITLVN
 YKNTPEWDEEVLKLTGGVGVDLVVENGGTGS
 LVK SMRCTRRGGVVSQVGYLGKQDPSE
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 /protein-id="CAK47188.1"
 /db-xref="GI:134084155"
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 /locus-tag="An18g011100"

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 intron complement(31046..31080
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34080..34956,
35015..35044,
35095..>35477))
CDS       complement (join (33419.. /locus-tag="An18g01120"
33465,33522..34023,
34080..34956,
35015..35044,
35095..35477))

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/inference="profile:COGS:COG2303"
/inference="profile:PFAM:PF00732"
/inference="profile:PFAM:PF05199"
/note="unnamed protein product;
Catalytic activity: versicolorin B
synthase from A. parasiticus
catalyses the side chain
cyclization of racemic versiconal
hemiacetal to the bisfuran ring
system of (-)-versicolorin B.
Pathway: versicolorin B synthase
from A. parasiticus is involved in
the aflatoxin biosynthetic
pathway. Remark: a splice site was
detected upstream of the START
codon. Remark: aflatoxins comprise
a group of polyketide-derived
carcinogenic mycotoxins. Remark:
the genes encoding the aflatoxin
biosynthetic enzymes in A.
parasiticus are clustered. Remark:
versicolorin B synthase from A.
parasiticus possesses an
amino-terminal sequence homologous
to the ADP-binding region of other
flavoenzymes, but does not require
flavin or nicotinamide cofactors
for its cyclase activity.
Similarity: the predicted A. niger
protein shows strong similarity to
versicolorin B synthase from A.
parasiticus and other
oxidoreductases. Title: strong
similarity to versicolorin B
synthase vbs - Aspergillus
parasiticus"
/citation=[30]
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VAEVPADVLPGVSDPETAAAHDW
GFVAENVPGANGRSIH YARGKCGGSSAMNFMII
QRPTIESMEQWATAVNDSSYTFDQ
TLPFYKNSVKFTPPNTQIRAKNATAGYDPSAYES
TGGPLKVS YANYAMPFSTWMDLGM

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KAIGINETQDFNLGSLMGQYCASTIDPNGEVRS
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 GAFQSPQLLMVSGVGPQDQLEEHG
 IQVVANRPVGQGNMWDHPFFAPSRYRVNVQTFTAI
 ANDFLGIVGQFINMVGFGNGPLTN
 PISDYLAWEKIPALRSASFSSQTTQLATFPSDW
 PEAEYISGAGYMGVNSNLLINQFE
 DGYQYASMLAVLITFTSRGNITLRSADTDDLPIV
 NPNWLATQSDQEVAIAMFKRVRAA
 FQSKAMAPVIIGNEYNPGLVQSDQEQILQWIKDN
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               35015..35044,
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CDS            37406..38455 /locus-tag="An18g01130"

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 Remark: the patent does not
 provide further information about
 the function of the protein.
 Similarity: the predicted A. niger
 protein shows similarity to the
 protein fragment (SEQ ID NO:

51484) of patent EP1033405-A2 from A. thaliana (AC# AAG41385) and to putative sterol desaturase family proteins. Title: similarity to protein fragment SEQ ID NO:51484 from patent EP1033405-A2 - Arabidopsis thaliana"

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LIAIHQLQVMRRMGHVLGFLDGDQHGDRGVPDVG
VAKVVRSLISTSTFRPIMTVFLSY
RVSQAPAQMSWGWLPLEIGLYGIILDFWFWYHHR
LMHDVGSGLWKYHRTTHLTKHPNPL
LTLYADTEQEFDFDIAGIPLMTYFSRLMGMPMGF
YEWWICHQYVVFTELAGHSGLRMH
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mat-peptide	38877..39833	/locus-tag="An18g01140"
		/product="unnamed"
exon	38805..39836	/locus-tag="An18g01140"
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mRNA	join(<40728..41152,	/locus-tag="An18g01150"

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42401..>42671)
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41226..42344,
42401..42671)

/locus-tag="An18g01150"

/inference="profile:COGS:COG0477"
/inference="similar to AA
sequence:UniProtKB:AF188621.1"
/note="unnamed protein product;
Function: FLU1 of C. albicans
facilitates resistance to
fluconazole and cycloheximide in
the fluconazole-hypersensitive S.
cerevisiae strain YKKB-13 lacking
the ABC (ATP-binding cassette)
transporter gene PDR5. Function:
FLU1 of C. albicans facilitates
resistance to mycophenolic acid in
C. albicans. Function: FLU1 of C.
albicans is involved in the
resistance to azol derivatives in
C. albicans. Function: MDR1 of C.
albicans facilitates resistance to
the anti-mitotic drug benomyl and
to the dihydrofolate reductase
inhibitor methotrexate.
Similarity: the predicted A. niger
protein shows strong similarity to
fluconazole resistance protein
FLU1of C. albicans, which is a
permease belonging to the major
facilitator superfamily. Title:
strong similarity to fluconazole
resistance protein FLU1 - Candida
albicans"
/citation=[59]
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WELGTKIYISAILAFTSICSTFDS
AIFSSSTTNVARVFGVIEVATLSSSLYICGYAS
GPLVWAPLSELKGRKPPIIVAMLG
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VAAVFSDIYNNRTRGVAIAMFST
VFLGPLLAPFIGGFINTSYLGWRWTAYIPAFMGY
AAFVLNMFLLKESYPPPIILVSKAS
ELRRRTKNWGIHAKQEEIEVDLRELLVNNFSRPL
RLLFGEPLILAVTIYLSFIYGLLY
CFLTAYTLVFQGYGMSAGVGGTLFGMVVGLFI
AASYIIFASRGYNKKLEANGGIPV
PEWRLPPVIIGGALFAGGLFWFGWTGFTKSIHWI
VPTLSGLFTGLGLLIIFIQLFNLY
IDTYLMFAASAIAANTFCRSLVAASFPLFSRQMF
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VAEH"
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exon 40728..41152

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exon	42401..42671	/number=2 /locus-tag="An18g01150"
gene	42950..43033	/number=3 /gene="tRNA-His (GTG)" /locus-tag="An18e01160"
tRNA	42950..43033	/gene="tRNA-His (GTG)" /locus-tag="An18e01160" /product="tRNA-His" /inference="profile:tRNAscan:1.4" /note="codon recognized: CAC"
gene	<43783..>45994	/locus-tag="An18g01170"
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/EC-number="2.4.2.30"
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 /inference="profile:PFAM:PF02877"
 /note="unnamed protein product;
 Catalytic activity: the NAP
 protein of Z. mays catalyses the
 reaction NAD(+) +
 {ADP-D-ribosyl}(N)-acceptor <=>
 nicotinamide +
 {ADP-D-ribosyl}(N+1)-acceptor.
 Function: the NAP protein of Z.
 mays is involved in programmed
 cell death or apoptosis.
 Localization: the NAP protein of
 Z. mays is a nuclear enzyme.
 Remark: the ADP-D-ribosyl group of
 NAD(+) is transferred to an
 acceptor carboxyl group on a
 histone or the enzyme itself, and
 further ADP-ribosyl groups are
 transferred to the 2'-position of
 the terminal adenosine moiety,
 building up a polymer with an
 average chain length of 20-30
 units. Remark: the NAP
 polynucleotide sequences can be
 used for modulation of programmed
 cell death in eukaryotic cells.
 the method is used, specifically
 in plants, to induce, or protect
 against, programmed cell
 death, depending on the extent to
 which FARP activity is reduced.

reducing expression of endogenous
 NAP class PARP only is also used
 to modulate programmed cell death,
 to increase growth rate and to
 produce plant cells that are more
 tolerant of stress (cold, chemical
 treatments, pathogens, pests,
 drought, heat, etc. , or during
 transformation). particular
 applications are generation of fungi
 plants that are resistant to fungi
 or nematodes; are male or female
 sterile ; or have better
 seed-shatter properties. the
 methods are also used to improve
 growth of transformed plant cells
 (and derived calli or complete
 plants). Similarity: the predicted
 A. niger protein shows st
 rong similarity to the protein
 sequence poly(ADP-ribose)
 polymerase NAP protein of patent
 WO200004173-A1 from Z. mays (AC#
 AAY68834) and from many other
 eucaryotic organisms. Title:
 strong similarity to
 poly(ADP-ribose) polymerase NAP
 protein from patent WO200004173-A1
 - Zea mays nucleus"
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 /citation=[63]
 /citation=[64]
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 LVESDSAGKKLDEKKFLMGSDIKK
 DDEPESPKKRTLEQALGINEDGTTKKLKDAQTVG
 TKQINVPVDDTCPLRLFTVYIDP
 TGLIWDATLNQTSATNNNNKFYRIQLLHRNNEFR
 TWTWGRVGEHGQHALLGGGGLDE
 AEYEFKKKPKDKSGLTWNRLDPPKKGKYTFIEK
 NYEEDTEDEDEDEKVVAKKPTKP
 KAEVVKCTLSAPVQDLVSFIFNKDFFQSTMASMS
 YDAQKLPLGKLSKRTLQNGFQALK
 DLSELIANPALASTKYDTSFTAAVEHLSNLYFTV
 IPHAFGRNRPPVLNNDNLLKREIE
 LLEALTDMEVANSIMKDARNTDTVHPLDRQFQGL
 NMQEMTPLEHTSTEFIELANYLNQ
 SRGHTHGVQYKVINIFRIERQGEKDRFQSSMYSN
 IQNSCRRLWHGSRSTNFGGILSQ
 GLRIAPPEAPVSGYMFKGQVYFADMSTKSAGYCF
 SWGSGNRGLLLLLCDVEVGNPMYER
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intron	43853..43911

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gene	<46879..>48537	/number=4
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/EC-number="3.5.1.11"
 /note="unnamed protein product;
 Function: penicillin V
 amidohydrolase (PVA) from F.
 oxysporum is used for the
 enzymatic hydrolysis of penicillin
 V (phenoxy-methylpenicillin) to
 6-aminopenicillanic acid (6-APA).
 6-APA is the active beta-lactam
 nucleus used in the manufacture of
 semi-synthetic penicillins.
 Similarity: the predicted A. niger
 protein shows strong similarity to
 the protein sequence penicillin V
 amidohydrolase (PVA) of patent
 US5516679-A from F. oxysporum (AC#
 AAW00291). Title: strong
 similarity to penicillin V
 amidohydrolase PVA from patent
 US5516679-A - Fusarium oxysporum
 extracellular/secretion proteins"
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 /db-xref="GI:134084161"
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 DDTVSVSVMWPLNNWNGRFOATGG
 GGLAAGIIGLAPHPVSQGYATAATDGGTLTLNGT
 SNPQTGAWILRPDGSINTALLLN
 AHRSIYDMTIIIGKTLTERFYGSPPRYSYWSGCST
 GGRQGYFAAAKYPNLFDFGLAGAP
 ALNFPRLIGYMFPPVHMFHSAAPPQCVDFTWFK
 AIIDECPLDGGATDGLISDYNPQS
 CPFKPEITLVGHTVTCTPEMGSDSPVTITAQHTLV
 KQILQGPDLQDHPDLWTGLPPGAS
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 PDYNVDFDMTDFDNTAYRLTLDGY
 NGILGSDDLNLSEFRAGGKLLTWHGLADELIPA

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intron        48455..48517      /locus-tag="An18g01180"
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exon          48518..48537      /locus-tag="An18g01180"
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gene          complement(48889..48960 /gene="tRNA-Ala (AGC)"
)
                                     /locus-tag="An18e01190"
tRNA          complement(48889..48960 /gene="tRNA-Ala (AGC)"
)
                                     /locus-tag="An18e01190"
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                                     /note="codon recognized: GCU"
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mRNA          join(<49850..49888,
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50419..50614,
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51538..>51919)
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CDS           join(49850..49888,
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51199..51470,
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                                     /inference="profile:PFAM:PF00067"
                                     /inference="similar to AA
sequence:UniProtKB:AFU81806.1"
                                     /note="unnamed protein product;
Function: ord1 of A. flavus
converts O-methylsterigmatocystin
to aflatoxin B1. Pathway: ord1 of
A. flavus catalyzes the last step
of the aflatoxin biosynthetic
pathway. Remark: aflatoxins
comprise a group of
polyketide-derived carcinogenic
mycotoxins. Similarity: the
predicted A. niger protein shows
strong similarity to
O-methylsterigmatocystin
(OMST)-oxidoreductase (ord1) from
A. flavus, which belongs to the
CYP64 family of cytochrome
P450-type monooxygenases. Title:
strong similarity to
O-methylsterigmatocystin
oxidoreductase ord1 - Aspergillus
flavus"

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LESRSSIHSSRPQQHFAEMAGWNNVLGAVKQSQR
FRATRKNLHREIGSNVSVARFNEI
QTAEVGRFLLRLVDAPDKLMKHIRKQWVGYYTIE
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TAFSDIPYAFVKEQMRTRGRFVPSF
LSNLLESSDLEPGSEENTVKWSAGSLYAGGADI
TVSSIASFFLAMALFPEVORKAQO
ELDTVIGTDRLPQYADREQLFYINALVKETFRWH
FVVFMSLTHTSADDVCEGYFIPK
GSSVLANIWAFTHDPAAYHDPMTFKPERFLSPKP
ERDPHFLVFGFGRVCPGRTLADV
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/exon 51199..51470 /locus-tag="An18g01200"
/intron 51471..51537 /locus-tag="An18g01200"
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52984..53309,
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52635..52939,
52984..53309,
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/inference="profile:PFAM:PF00069"
/note="unnamed protein product;
Function: SRPK2 from M. musculus
phosphorylates SF2/ASF, a member
of SR splicing factors. Remark:
overexpression of murine SRPK2
causes disassembly of
cotransfected SF2/ASF and
endogenous SC35. SRPK family
members may regulate the
disassembly of the SR proteins in
a tissue-specific manner.
Similarity: the predicted A. niger
protein shows similarity to SRPK2
from M. musculus and strong
similarity to putative
serine/threonine protein kinases
from several eucaryotic organisms.
Title: similarity to
SR-protein-specific kinase SRPK2 -
Mus musculus nucleus"
/citation={39}
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LGYGVTSTVMGLGRDLRDSKYVVLKIYVTGQEKNH
ELEIYNRMNAVEVEHPGRDLVRRRL
FDHFTVIGPHGPHVCLVHEPMGMSADTLQKYIP
GNTMTLDEMKTICIRQLLIALDFLH
SAARIVHTGKDLQLKNLLLPVPNTKTLELEERE
VNDPSPRKILKDRTIYLSVTYNFG
GSGPLISDFGEARFGDVEKRDDIMPNMYRAPEV
VLKENWNYKVVDIWNVAMVAVDIVI
PRHMFDRGNADGIFDDRVHIAEMIALMGPPPASF
RERCRLAYVFWDQGNWKLAPIP
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exon      complement(53368..53720 /number=4
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gene      complement(<54105..>557 /number=5
62) /locus-tag="An18g01220"

mRNA      complement(join(<54105. /locus-tag="An18g01220"
.54731,54787..55334,
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55559..>55762))

CDS       complement(join(54105.. /locus-tag="An18g01220"
54731,54787..55334,
55392..55500,
55559..55762))

/inference="profile:COGS:COG0477"
/inference="similar to AA
sequence:PIR:S64826"
/note="unnamed protein product;
Function: in S. cerevisiae,
mutants (dal5) that lack
allantoate transport have been
isolated. these strains also
exhibit a 60% loss of allantoin
transport capability. Regulation:
in S. cerevisiae Dal5 appears to
be sensitive to nitrogen
catabolite repression, feedback
inhibition, and trans-inhibition.
Regulation: in S. cerevisiae
allantoate uptake is constitutive.
Similarity: the predicted A. niger
protein shows strong similarity to
allantoate permease gene (DAL5)
from S. cerevisiae, which belongs
to the major facilitator
superfamily. Title: strong
similarity to allantoate permease
Dal5 - Saccharomyces cerevisiae"
/citation=[7]
/citation=[9]
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/db-xref="GI:134084164"
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PNIYCLQKVPAAKWLGVNVALWGVAAAASAGAKN
YATLLTARVFLGIFEATIGPSLML
ISSQYYTKSEQAPRFTLWYNGLVQAIIIGLVSF
GFQYVHHGATLAGWRIMFLVIGLV
TVLIGVLTLLFIPDTPMKAKWLSSEEVALLQHV
SVNQGTGVWSSAINLKQIWEQVLDI
QLWLLVLITILISVSSGVVITYSATLIAGFGYS
PISALLNMPSGIVSIFPTLLVGFG
IRRTSHRWAWNAFCTIPGIIGGLLSFLPKSNKA

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GVLIGIYLVNAIVATLPILYQWTM
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 DKENTRFRFVY"

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intron    complement(54732..54786 /locus-tag="An18g01220"
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)
exon      complement(55392..55500 /locus-tag="An18g01220"
)
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)
gene      <56384..>58444
mRNA      join(<56384..56645,
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57069..57368,
57430..57711,
57897..58158,
58326..58444)

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/note="unnamed protein product;
 Function: M. grisea Pth11 is a
 pathogenicity gene. Function: M.
 grisea Pth11p likely is involved
 in host surface recognition.
 Function: M. grisea pth11 mutants
 of strain 4091-5-8 are
 nonpathogenic due to a defect in
 appressorium differentiation.
 Localization: in M. grisea, a
 Pth11-green fluorescent protein
 fusion localised to the cell
 membrane and vacuoles. Similarity:
 similarity of the predicted A.
 niger protein and M. grisea Pth11
 is limited to the N-terminal half
 of the protein sequences. Title:
 similarity to integral membrane
 protein PTH11 - Magnaporthe grisea
 plasma membrane"
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mRNA	join(<59070..59441, 59521..59806, 59879..60178, 60237..60312, 60374..>60560)	/locus-tag="An18g01240"
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/inference="profile:COGS:COG0654"
 /inference="profile:PFAM:PF01360"
 /note="unnamed protein product;
 Catalytic activity: NahW of P.

stutzeri catalyzes the conversion
salicylate + NADH + O(2) <=>
catechol + NAD(+) + H(2)O + CO(2).
Pathway: NahW of P. stutzeri is
involved in the metabolization of
naphtalene and salicylates (lower
naphtalene degradation pathway).
Similarity: the predicted A. niger
protein shows similarity to
salicylate hydroxylase (nahW) of
P. stutzeri, which belongs to the
NADH-dependent monooxygenase
superfamily. Title: similarity to
salicylate hydroxylase nahW
-Pseudomonas stutzeri"
/citation=

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sequence:PIR:S45605"

/note="unnamed protein product;
Catalytic activity: alcohol + NAD+
= aldehyde or ketone + NADH.
Pathway: alcohol dehydrogenase
ADH-T from B. stearothermophilus
is involved in glycolysis /
gluconeogenesis; fatty acid
metabolism; bile acid
biosynthesis; tyrosine metabolism;
glycerolipid metabolism. Remark:
the protein sequence of alcohol
dehydrogenase ADH-T from B.
stearothermophilus NCA1503 is
covered by patent JP04218378-A
(AC# AAR26874). Similarity: the
predicted A. niger protein shows
strong similarity to thermostable
alcohol dehydrogenase ADH-T from
B. stearothermophilus NCA1503,
which belongs to the zinc alcohol
dehydrogenase (ADH) family. Title:
strong similarity to thermostable
alcohol dehydrogenase adhT -
Bacillus stearothermophilus"
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KRAYGQHDFDVGFSFSGTVDADAVYPIPEGYDS
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SDRVGVMIGGLGHLAIKLARALRYNVVALSSSE
KKREEALEFGASEFYRFPNTQTPN
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CDS	join(101875..101958, 102203..102219, 102259..102360, 102392..102399, 102621..103153, 103205..104542)	/locus-tag="An18g01440"

/inference="profile:COGS:COG3496"
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 Similarity: the predicted A. niger
 protein shows local similarity to
 the hypothetical protein ml18086
 from M. loti. Title: strong
 similarity to hypothetical protein
 CAD70872.1 - Neurospora crassa"
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 IKSLSKDKSVIGKPLLFPTILDHT
 RLSPIKNNFTFNVLFVGVIGVISCRFGRLLSIDA
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 WFSFDSARYLHRGDDTSLNKLNKFLREQNENP
 AKWPYAYMLSVPRFLWWERSVVTW
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 RIYTESPEKGFEQLLDCKEEHLDE
 DKRVFSLIPQHGKYAYKATWKKEIFSSPFKEVGE
 TVSSFTLDPVVPSSWSGNRSLNT
 TTFDPGAPRMRIARLWCKVPPIDPGKASSQIFS
 ILLIWTNVNVTALPRILFQAIRLH
 VMNLMRMMEHPDVRPGSEPRRPSKGERKDAPLKM
 LHSFLDLHANLQSRMLERFFREYL
 KHIVASYPGDLEVITYIPCKSVFKTTICLRSTQYS
 AEGQDPRRLRLLEVMDPAFYSRIVN
 SPNAGTAMAKETKPGRSPADALSSPVIASDITQS
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intron	102361..102391	/number=3
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gene	<106231..>106803	/number=6
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CDS	join(106231..106565, 106647..106803)	/locus-tag="An18g01450"

/EC-number="1.14.-.-"
 /note="unnamed protein product;
 Function: ordA of A. parasiticus
 is involved in the aflatoxin
 biosynthesis and converts
 O-methylsterigmatocystin (OMST) to
 aflatoxins B1 or G1 and converts
 dihydro-O-methylsterigmatocystin
 (DHOMST) to aflatoxins B2 or G2.
 Remark: aflatoxins comprise a
 group of polyketide-derived
 carcinogenic mycotoxins. Remark:
 it is assumed that the ORF is
 N-terminally shorter and has
 another start codon 5' to the
 predicted one ; the ORF is around
 400 amino acids shorter than most
 of the homologues cytochrome p450
 proteins. Remark: ordA of A.
 parasiticus is also called
 cytochrome p450 64, cyp64 or omst
 oxidoreductase. Similarity: the
 ORF shows similarity to several
 cytochrome P450 related proteins
 from different species. Title:
 strong similarity to
 O-methylsterigmatocystin
 oxidoreductase ordA - Aspergillus
 parasiticus"
 /citation=[43]
 /codon-start=1
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 HNLAFGFGRRICPGRGFADSTIFL
 TVVRSLQAFRIAKISEDGREIEPIVEYLPGVISH
 PKPFAISITPRSKHEHSFIRSIEI
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 /number=1

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intron	106566..106646	/locus-tag="An18g01450"
exon	106647..106803	/number=1
gene	<107279..>108340	/locus-tag="An18g01450"
mRNA	join(<107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..>108340)	/number=2
CDS	join(107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..108340)	/locus-tag="An18g01460"
		/EC-number="1.-.-." /inference="profile:COGS:COG1028" /inference="profile:PFAM:PF00106" /notes="unnamed protein product; Catalytic activity: cyclohexanol dehydrogenases convert cyclohexanol + NAD(+) <=> cyclohexanone + NADH. Function: chnA of A. sp. is an alcohol dehydrogenases proposed to catalyze the conversion of cyclohexanol to cyclohexanone (EC 1. 1. 1. 245). Phenotype: cyclohexanol was detected as the major intermediate accumulated in the chnA mutant of A. sp. Remark: chnA of A. sp. is encoded in the gene cluster for cyclohexanol oxidation. Similarity: the ORF shows similarity to several dehydrogenases from different species and with various specificities. Title: strong similarity to cyclohexanol dehydrogenase chnA - Acinetobacter sp" /citation=[57] /codon-start=1 /protein-id="CAK47219.1" /db-xref="GI:134084186" /translation="MAHLLQGTAFIGAGSGIGA GVARTFIQNGISKALVDINLSIL QKVSESLKQTFPNVELLTSADVVTNEVHVDNAVQ KAATTFRGRVDIGVNSAGVGDGPEP TDRLSLKDWQRTVHINQTVGWLSQLIQQMLTQ KSRGTRHGRGVIVNVCCSSLGITAS ATGIPFPAYTSSKHGVMGLTKMDAKYYAPSGIRI NAVCPGFVDTPMVSKAVDSGVFKK EVESAPVGRIGDVEEITDSILFLASPMSSFIYGA GLVVDGGYGL" /locus-tag="An18g01460" /inference="protein motif:SignalP:2.0" /locus-tag="An18g01460"
sig-peptide	join(107279..107327, 107380..107387)	
mat-peptide	join(107388..107740,	

	107795..107907, 107966..107988, 108045..108097, 108151..108337)	
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intron	107741..107794	/locus-tag="An18g01460" /number=2
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intron	108098..108150	/locus-tag="An18g01460" /number=5
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gene	<108826..>111209	/locus-tag="An18g01470"
mRNA	join(<108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960, 111135..>111209)	/locus-tag="An18g01470"
CDS	join(108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960, 111135..111209)	/locus-tag="An18g01470"
		/EC-number="1.14.-.-" /inference="profile:COGS:COG0493" /note="unnamed protein product; Remark: aflatoxins are polyketide-derived secondary metabolites. Remark: moxY of A. parasiticus is expressed concurrently with genes involved in aflatoxin biosynthesis and it lies on one end of the cluster of this genes. Therefore moxY of A. parasiticus is presumably also

involved in aflatoxin biosynthesis. Similarity: the ORF shows similarity to monooxygenases from several species and with different functions. Title: strong similarity to monooxygenase moxY -Aspergillus parasiticus"
/citation=[55]
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PSFGGTWYFNKCCGVDIPAAFYSFALYPQFTC
FFPKQEEILQYIHGVADEFVSLK
LVGHTEWEGADWDSEQCWEVRLREIPSGRKFT
RCRILISAVGGGLTNPKHVMLQGIE
RFQGNIVHTALWDQETAVAGKNVIVIGNASATQ
FIPAADDAASINQFIRHVRKCAP
EEQYWSLLTPEYSIGCKRRVFDNDGYLKCLHRPN
VDIINDPVAVEEQSITTQSGKRF
PADLIADVLDYGRCLRLGSLRSTMTSTGEVVMG
VRDNIGTVAAYKHLRRWPWRNF
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intron	109024..109088
exon	109089..109305
intron	109306..109376
exon	109377..109778
intron	109779..109840
exon	109841..109905
intron	109906..110159
exon	110160..110181
intron	110182..110243
exon	110244..110293
intron	110294..110354
exon	110355..110492
intron	110493..110523
exon	110524..110752

intron	110753..110865	/locus-tag="An18g01470"
exon	110866..110960	/number=9
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		/number=10
intron	110961..111134	/locus-tag="An18g01470"
		/number=10
exon	111135..111209	/locus-tag="An18g01470"
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gene	<111907..>113460	/locus-tag="An18g01480"
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		/inference="similar to AA
		sequence:UniProtKB:AB013443.1"
		/note="unnamed protein product;
		Function: eln2 of C. cinereus
		encodes a novel type of microsomal
		cytochrome P450 enzyme, with is
		involved in mushroom
		morphogenesis. Phenotype: a
		dominant mutation of the
		elongationless2 (eln2) gene of the
		mushroom C. cinereus affects
		pattern formation in the
		development of fruit body
		primordia, causing dumpy primordia
		which culminate in mature fruit
		bodies with short stipes.
		Similarity: the ORF shows
		similarity to several cytochrome
		p450 related proteins from
		different species, which have
		different cellular functions.
		Title: strong similarity to
		cytochrome p450 related protein
		eln2 - Coprinus cinereus"
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		/codon-start=1
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		IARDLLDKRGSYADRPDLVMANN
		ITKGLHMLIRQYDDWLRHLHQRLDAPLLSPRASNT
		YHPIQDLESQQLMFDDLRSNDFDA
		HFERYSGSLMFALAYGFRLLSPKGQELRDMRTIQ
		GNFTYAAARVGTWIVDAIPVLNLYLP
		AVVAPWKRLEKLFKLEASVHTRHLEKGLNSEPW
		NWSKEFAASKHAEQMPRLDLAYNL
		GILVDAGFETTWTVMKIFVLAMRSDPRFVAVARK
		ELDEVVGEDRMPTFEDQEKLVYIQ
		AVVDETLRWRSMAPGGIPHAARKEDTYMGYRIPK
		GATVIFPLFWSMCLTDEPDDPLEF
		RPERWFEATEKEEGRFRNFYFGYRRICTRGRIAR
		NSLFLLMARILWAFDIAQPLGDDG
		KPVVPDDMAFDSAFVSTPEPFALFVPRSEKTEK
		IVEREWNEMEKDMAVLMGQVRDSQ
		RALGLDVRA"
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		/inference="protein

mat-peptide	111958..113457	motif:SignalP:2.0" /locus-tag="An18g01480"
exon	111907..113460	/product="unnamed" /locus-tag="An18g01480"
gene	complement(<113565..>114733)	/number=1 /locus-tag="An18g01490"
mRNA	complement(join(<113565..114153, 114210..>114733))	/locus-tag="An18g01490"
CDS	complement(join(113565..114153, 114210..114733))	/inference="profile:COGS:COG0598" /inference="profile:PFAM:PF01544" /inference="similar to AA sequence:UniProtKB:SC41293.1" /note="unnamed protein product; Function: alr2 of S. cerevisiae is an uptake transporter for inorganic cations, e. g. magnesium, which presence seems to be important for resistance to the toxic effect of aluminum. Remark: alr2 of S. cerevisiae is also called YFL050C. Similarity: the predicted ORF is 395 amino acids shorter at the N-terminus and 57 amino acids shorter at its C-terminal end than alr2 of S. cerevisiae (nearly the same is true for alr1 of S. cerevisiae). Title: strong similarity to ion transporter Alr2 -Saccharomyces cerevisiae plasma membrane" /citation=[40] /codon-start=1 /protein-id="CAK47222.1" /db-xref="GI:134084189" /translation="MSSDSTPDPRLEKPRVAVAS RLNFFTSQNLNTSIEASSIEDLCSV YRPFELLETTGAHSGLWLLDITAPSEEDIEALAR FFNLHPLTTEDIKTRETRKIELF GQYYFLSLRPPRRLETDIGVRIVSHNLYAVVFRG GVLSFSFDPSSLHTSHVRQRIKEHS SHLLTSDWICYALIDDIVDGFAPFISRVENGVV TVEDSVSITRPDDMGLALQRIKFL RKEVMNIRQPLHDKIDVIRSFARHCDISDTSSSQ VALYLSDDICDHVVMTIANLEQAEQ MLSRLOQSKYLTQVHFDSGRMRNGIASLSKLTVL ASILVPMQFITGLGFNMNVRVPGKT HDGDNLSLTWWFSILGFILGLTVIFAWAKRIGLL DR"
exon	complement(113565..114153)	/locus-tag="An18g01490"
intron	complement(114154..114209)	/number=1 /locus-tag="An18g01490"
exon	complement(114210..114733)	/number=1 /locus-tag="An18g01490"
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gene complement(<115549..>11 /locus-tag="An18g01500"
6444)
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INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:55:47 ON 07 JUL 2008
SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND? AND CD4+ CELL? AND

0* FILE ADISCTI
SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND? AND CD4+ CELLS

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SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND?

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2 FILE CAPLUS
0* FILE CEABA-VTB
0* FILE CIN
0* FILE ESBIOBASE
0* FILE FOMAD
0* FILE FOREGE
2* FILE FROSTI
0* FILE FSTA
5 FILE GENBANK
1 FILE IFIPAT
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
1* FILE PASCAL
0* FILE PHARMAML
1 FILE SCISEARCH
1 FILE TOXCENTER
21 FILE USPATFULL
3 FILE USPAT2
0* FILE WATER
2 FILE WPIDS
2 FILE WPINDEX

L1 QUE LACTOBACILLUS REUTERI AND TOXIN(P) BIND?

FILE 'BIOTECHDS, CAPLUS, FROSTI, GENBANK, IFIPAT, PASCAL, SCISEARCH,
TOXCENTER, USPATFULL, USPAT2' ENTERED AT 13:59:37 ON 07 JUL 2008

L2 38 S L1
L3 34 DUP REM L2 (4 DUPLICATES REMOVED)
L4 27 S L3 AND (TABLET OR FOOD OR DIETARY SUPPLEMENT OR CONFECTIONERY
L5 27 DUP REM L4 (0 DUPLICATES REMOVED)

=> d 15 1

L5 ANSWER 1 OF 27 USPATFULL on SIN
AN 2007:296111 USPATFULL
TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface

protein homologues and uses therefore

IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
 Altermann, Eric, Palmerston North, NEW ZEALAND
 Buck, B. Logan, Banner Elk, NC, UNITED STATES
 Russell, W. Michael, Newburgh, IN, UNITED STATES

PA North Carolina State University, Raleigh, NC, UNITED STATES (U.S. corporation)

PI US 20070258955 A1 20071108
 AI US 2007-701335 A1 20070201 (11)

RLI Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING

PRAI US 2003-465621P 20030425 (60)

DT Utility

FS APPLICATION

LN.CNT 5104

INCL INCLM: 424/093.400
 INCLS: 435/252.100; 435/252.900; 435/320.100; 435/006.000; 435/007.100;
 435/070.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100

NCL NCLM: 424/093.400
 NCLS: 435/006.000; 435/007.100; 435/070.100; 435/252.100; 435/252.900;
 435/320.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100

IC IPCI A61K0035-00 [I,A]; A61K0038-00 [I,A]; A61P0001-00 [I,A];
 C07H0021-02 [I,A]; C07H0021-00 [I,C*]; C07K0016-00 [I,A];
 C07K0004-00 [I,A]; C12N0001-20 [I,A]; C12N0015-00 [I,A];
 C12P0021-04 [I,A]; C12Q0001-68 [I,A]

IPCR A61K0035-00 [I,C]; A61K0035-00 [I,A]; A61K0038-00 [I,C];
 A61K0038-00 [I,A]; A61P0001-00 [I,C]; A61P0001-00 [I,A];
 C07H0021-00 [I,C]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
 C07K0004-00 [I,C]; C07K0004-00 [I,A]; C07K0014-195 [I,C*];
 C07K0014-335 [I,A]; C07K0016-00 [I,C]; C07K0016-00 [I,A];
 C12N0001-20 [I,C]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
 C12N0015-00 [I,C]; C12N0015-00 [I,A]; C12P0021-04 [I,C];
 C12P0021-04 [I,A]; C12P0021-06 [I,C*]; C12P0021-06 [I,A];
 C12Q0001-68 [I,C]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 2

L5 ANSWER 2 OF 27 USPATFULL on STN

AN 2007:197155 USPATFULL

TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface protein homologues and uses therefore

IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
 Altermann, Eric, Palmerston North, NEW ZEALAND
 Buck, B. Logan, Banner Elk, NC, UNITED STATES
 Russell, W. Michael, Newburgh, IN, UNITED STATES

PA North Carolina State University, Raleigh, NC, UNITED STATES, 27695-8210 (U.S. corporation)

PI US 20070172495 A1 20070726
 AI US 2007-701319 A1 20070201 (11)

RLI Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING

PRAI US 2003-465621P 20030425 (60)

DT Utility

FS APPLICATION

LN.CNT 5104

INCL INCLM: 424/234.100
 INCLS: 514/044.000; 435/006.000; 435/007.320; 435/069.100; 435/252.900;
 435/471.000; 530/350.000; 536/023.700

NCL NCLM: 424/234.100
 NCLS: 435/006.000; 435/007.320; 435/069.100; 435/252.900; 435/471.000;
 514/044.000; 530/350.000; 536/023.700

IC IPCI A61K0048-00 [I,A]; A61K0039-02 [I,A]; C12Q0001-68 [I,A];
G01N0033-554 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*];
C12P0021-06 [I,A]; C07K0014-335 [I,A]; C07K0014-195 [I,C*];
IPCR A61K0048-00 [I,C]; A61K0048-00 [I,A]; A61K0039-02 [I,C];
A61K0039-02 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];
C07K0014-195 [I,C]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
C12P0021-06 [I,C]; C12P0021-06 [I,A]; C12Q0001-68 [I,C];
C12Q0001-68 [I,A]; G01N0033-554 [I,C]; G01N0033-554 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 3

L5 ANSWER 3 OF 27 USPATFULL on SIN
AN 2007:140436 USPATFULL
TI Delivery of trefoil peptides
IN Hane, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
Steidler, Lothar, Lokeren, BELGIUM
Remaut, Erik Rene, Lovendegem, BELGIUM
PI US 20070122427 A1 20070531
AI US 2007-654879 A1 20070118 (11)
RLI Division of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A 371
of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000
PRAI EP 1999-870143 19990705
DT Utility
FS APPLICATION
LN.CNT 1335
INCL INCLM: 424/200.100
INCLS: 435/252.300; 435/252.900
NCL NCLM: 424/200.100
NCLS: 435/252.300; 435/252.900
IC IPCI A61K0039-02 [I,A]; C12N0001-21 [I,A]
IPCR A61K0039-02 [I,C]; A61K0039-02 [I,A]; C12N0001-21 [I,C];
C12N0001-21 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 4

L5 ANSWER 4 OF 27 USPATFULL on SIN
AN 2007:134502 USPATFULL
TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
(non-U.S. corporation)
PI US 20070117183 A1 20070524
AI US 2006-511140 A1 20060828 (11)
RLI Division of Ser. No. US 2005-55822, filed on 11 Feb 2005, PENDING
Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED
PRAI DE 1999-19932125 19990709
DE 1999-19932227 19990709
DE 1999-19932228 19990709
DE 1999-19932230 19990709
DE 1999-19933005 19990714
DE 1999-19933006 19990714
DE 1999-19940764 19990827
DE 1999-19940766 19990827

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DE	1999-19942124	19990903
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DE	1999-19933004	19990714
DE	1999-19940765	19990827
DE	1999-19941380	19990831
DE	1999-19941394	19990831
DE	1999-19942076	19990903
DE	1999-19942086	19990903
DE	1999-19942095	19990903
DE	1999-19942129	19990903
US	1999-141031P	19990625 (60)
US	1999-142101P	19990702 (60)
US	1999-148613P	19990812 (60)
US	2000-187970P	20000309 (60)
DT	Utility	
FS	APPLICATION	
LN.CNT	8386	
INCL	INCLM: 435/069.100	
	INCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;	
	536/023.200	
NCL	NCLM: 435/069.100	
	NCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;	
	536/023.200	
IC	IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12P0021-06 [I,A];	
	C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];	
	C12N0009-10 [I,A]; C12N0015-74 [I,A]; C12N0001-21 [I,A]	

IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C];
C12N0001-21 [I,A]; C12N0009-10 [I,C]; C12N0009-10 [I,A];
C12N0015-74 [I,C]; C12N0015-74 [I,A]; C12P0013-00 [I,C];
C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0021-06 [I,C];
C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 6

L5 ANSWER 6 OF 27 USPATFULL on SIN
AN 2007:130427 USPATFULL
TI Delivery of trefoil peptides
IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
Steidler, Lothar, Lokeren, BELGIUM
Remaut, Erik Rene, Lonendegem, BELGIUM
PA Vlaams Interuniversitair Instituut voor Biotechnologie, BELGIUM
(non-U.S. corporation)
PI US 7220418 B1 20070522
WO 2001002570 20010111
AI US 2000-30390 20000705 (10)
WO 2000-EP6343 20000705
20020416 PCT 371 date
PRAI EP 1999-870143 19990705
DT Utility
FS GRANTED
LN.CNT 1334
INCL INCLM: 424/200.100
INCLS: 424/093.450; 424/093.200; 424/234.100; 424/192.100; 514/925.000
NCL NCLM: 424/200.100
NCLS: 424/093.200; 424/093.450; 424/192.100; 424/234.100; 514/925.000
IC IPCI A01N0063-00 [I,A]; A61K0039-02 [I,A]; A61K0039-00 [I,A]
IPCR A01N0063-00 [I,C]; A01N0063-00 [I,A]; C12N0015-09 [I,C*];
C12N0015-09 [I,A]; A61K0035-66 [I,C*]; A61K0035-74 [I,A];
A61K0038-00 [I,C*]; A61K0038-00 [I,A]; A61K0039-00 [I,C];
A61K0039-00 [I,A]; A61K0039-02 [I,C]; A61K0039-02 [I,A];
A61K0048-00 [I,C*]; A61K0048-00 [I,A]; A61P0001-00 [I,C*];
A61P0001-04 [I,A]; C07K0014-435 [I,C*]; C07K0014-575 [I,A];
C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0015-16 [I,C*];
C12N0015-16 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
C12R0001-01 [N,A]
EXF 424/200.1; 424/192.1; 424/184.1; 424/234.1; 424/244.1; 424/246.1;
424/93.2; 424/93.45; 514/2; 514/925; 435/69.3; 435/69.1; 435/71.1;
435/252.9

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 7

L5 ANSWER 7 OF 27 IFIPAT COPYRIGHT 2008 IFI on SIN
AN 11053905 IFIPAT;IFIUDB;IFICDB
TI METHOD OF IMPROVING IMMUNE FUNCTION IN MAMALS USING LACTOBACILLUS
REUTERI STRAINS
IN Kang Ho-Jin (KR); Kwon Ik-boo (KR); Lee Dong-Seog (KR); Mollstam Bo (SE)
PA Unassigned Or Assigned To Individual (68000)
PI US 2006002907 A1 20060105
AI US 2002-531651 20021018
WO 2002-SE1903 20021018
20050415 PCT 371 date
20050415 PCT 102(e) date
FI US 2006002907 20060105
DT Utility; Patent Application - First Publication

FS CHEMICAL
APPLICATION
ED Entered STN: 9 Jan 2006
Last Updated on STN: 9 Jan 2006
CLMN 9
GI 1 Figure(s).

FIG. 1. Confirmation of inhibitory ability against the binding of vero cytotoxin(VT) and Gb3 receptor in a culture supernatant of L. reuteri through competitive ELISA. Each reacted as follows, on plates coated with Gb3, followed by performing ELISA using mAb against VT.

=> d 15 8

L5 ANSWER 8 OF 27 USPATFULL on STN
AN 2006:274450 USPATFULL
TI Gene products differentially expressed in cancerous cells
IN Scott, Elizabeth M., Emeryville, CA, UNITED STATES
Lamson, George, Emeryville, CA, UNITED STATES
Kassam, Altaf, Emeryville, CA, UNITED STATES
Zhang, Guozhong, Emeryville, CA, UNITED STATES
Sakamoto, Doreen, Emeryville, CA, UNITED STATES
Garcia, Pablo Dominguez, Emeryville, CA, UNITED STATES
May, Theresa, Emeryville, CA, UNITED STATES
Kennedy, Giulia C., Emeryville, CA, UNITED STATES
Kang, Sanmao, Emeryville, CA, UNITED STATES
Reinhard, Christoph, Emeryville, CA, UNITED STATES
Jefferson, Ann Bennett, Emeryville, CA, UNITED STATES
PA Chiron Corporation (U.S. corporation)
PI US 20060234246 A1 20061019
AI US 2004-934842 A1 20040902 (10)
RLI Continuation-in-part of Ser. No. US 2002-165835, filed on 6 Jun 2002,
ABANDONED Continuation of Ser. No. US 2000-490818, filed on 25 Jan 2000,
GRANTED, Pat. No. US 6429302 Continuation-in-part of Ser. No. US
2001-883152, filed on 15 Jun 2001, ABANDONED Continuation-in-part of
Ser. No. WO 2003-US15465, filed on 16 May 2003, PENDING
PRAI US 1999-118302P 19990202 (60)
US 2000-211835P 20000615 (60)
US 2003-445222P 20030204 (60)
US 2002-381533P 20020517 (60)
DT Utility
FS APPLICATION
LN.CNT 17024
INCL INCLM: 435/006.000
INCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
530/388.800; 536/023.500
NCL NCLM: 435/006.000
NCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
530/388.800; 536/023.500
IC IPCI C12Q0001-68 [I,A]; G01N0033-574 [I,A]; C07H0021-04 [I,A];
C07H0021-00 [I,C*]; C12P0021-06 [I,A]; C07K0014-82 [I,A];
C07K0016-30 [I,A]; C07K0016-18 [I,C*]
IPCR C12Q0001-68 [I,C]; C12Q0001-68 [I,A]; C07H0021-00 [I,C];
C07H0021-04 [I,A]; C07K0014-82 [I,C]; C07K0014-82 [I,A];
C07K0016-18 [I,C]; C07K0016-30 [I,A]; C12P0021-06 [I,C];
C12P0021-06 [I,A]; G01N0033-574 [I,C]; G01N0033-574 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 9

L5 ANSWER 9 OF 27 USPATFULL on STN

AN 2006:98984 USPATFULL

TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF

PA Habershauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
 (non-U.S. corporation)

PI US 20060084152 A1 20060420

AI US 2005-239674 A1 20050928 (11)

RLI Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED
 Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
 ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23
 Jun 2000, ABANDONED

PRAI DE 1999-19932125 19990709
 DE 1999-19932227 19990709
 DE 1999-19932228 19990709
 DE 1999-19932230 19990709
 DE 1999-19933005 19990714
 DE 1999-19933006 19990714
 DE 1999-19940764 19990827
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 DE 1999-19940832 19990827
 DE 1999-19941378 19990831
 DE 1999-19941379 19990831
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 DE 1999-19932229 19990709
 DE 1999-19941396 19990831
 DE 1999-19942087 19990903
 DE 1999-19930476 19990701
 DE 1999-19931419 19990708
 DE 1999-19931420 19990708
 DE 1999-19932206 19990709
 DE 1999-19942088 19990903
 DE 1999-19942124 19990903
 DE 1999-19932928 19990714
 DE 1999-19931415 19990708
 DE 1999-19931424 19990708
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 DE 1999-19931510 19990708
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 DE 1999-19931592 19990708
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 DE 1999-19931634 19990708
 DE 1999-19931636 19990708
 DE 1999-19932130 19990708
 DE 1999-19932186 19990709
 DE 1999-19932922 19990714
 DE 1999-19932926 19990714
 DE 1999-19933004 19990714

DE 1999-19940765 19990827
 DE 1999-19941380 19990831
 DE 1999-19941394 19990831
 DE 1999-19942076 19990903
 DE 1999-19942086 19990903
 DE 1999-19942095 19990903
 DE 1999-19942129 19990903
 DE 1999-19932124 19990709
 DE 1999-19932127 19990709
 DE 1999-19932133 19990709
 DE 1999-19932207 19990709
 DE 1999-19932208 19990709
 DE 1999-19932225 19990709
 DE 1999-19932914 19990709
 DE 1999-19940768 19990827
 DE 1999-19940831 19990827
 DE 1999-19941385 19990831
 US 1999-141031P 19990625 (60)
 US 1999-142101P 19990702 (60)
 US 1999-148613P 19990812 (60)
 US 2000-187970P 20000309 (60)
 US 1999-141031P 19990625 (60)
 US 1999-143694P 19990714 (60)
 US 1999-151778P 19990831 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 14822
 INCL INCLM: 435/113.000
 INCLS: 435/115.000; 435/252.300
 NCL NCLM: 435/113.000
 NCLS: 435/115.000; 435/252.300
 IC IPCI C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
 C12N0001-20 [I,A]
 IPCR C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];
 C12N0001-20 [I,A]; C12P0013-08 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 9

L5 ANSWER 9 OF 27 USPATFULL on SIN
 AN 2006:98984 USPATFULL
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
 PA Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
 (non-U.S. corporation)
 PI US 20060084152 A1 20060420
 AI US 2005-239674 A1 20050928 (11)
 RLI Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED
 Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
 ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23
 Jun 2000, ABANDONED
 FRAI DE 1999-19932125 19990709
 DE 1999-19932227 19990709
 DE 1999-19932228 19990709
 DE 1999-19932230 19990709
 DE 1999-19933005 19990714
 DE 1999-19933006 19990714

DE 1999-19940764	19990827
DE 1999-19940766	19990827
DE 1999-19940832	19990827
DE 1999-19941378	19990831
DE 1999-19941379	19990831
DE 1999-19942077	19990903
DE 1999-19942079	19990903
DE 1999-19931418	19990708
DE 1999-19932126	19990709
DE 1999-19932229	19990709
DE 1999-19941396	19990831
DE 1999-19942087	19990903
DE 1999-19930476	19990701
DE 1999-19931419	19990708
DE 1999-19931420	19990708
DE 1999-19932206	19990709
DE 1999-19942088	19990903
DE 1999-19942124	19990903
DE 1999-19932928	19990714
DE 1999-19931415	19990708
DE 1999-19931424	19990708
DE 1999-19931428	19990708
DE 1999-19931434	19990708
DE 1999-19931435	19990708
DE 1999-19931443	19990708
DE 1999-19931453	19990708
DE 1999-19931457	19990708
DE 1999-19931465	19990708
DE 1999-19931478	19990708
DE 1999-19931510	19990708
DE 1999-19931541	19990708
DE 1999-19931573	19990708
DE 1999-19931592	19990708
DE 1999-19931632	19990708
DE 1999-19931634	19990708
DE 1999-19931636	19990708
DE 1999-19932130	19990708
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DE 1999-19932922	19990714
DE 1999-19932926	19990714
DE 1999-19933004	19990714
DE 1999-19940765	19990827
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DE 1999-19941394	19990831
DE 1999-19942076	19990903
DE 1999-19942086	19990903
DE 1999-19942095	19990903
DE 1999-19942129	19990903
DE 1999-19932124	19990709
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DE 1999-19932207	19990709
DE 1999-19932208	19990709
DE 1999-19932225	19990709
DE 1999-19932914	19990709
DE 1999-19940768	19990827
DE 1999-19940831	19990827
DE 1999-19941385	19990831
US 1999-141031P	19990625 (60)
US 1999-142101P	19990702 (60)
US 1999-148613P	19990812 (60)
US 2000-187970P	20000309 (60)

US 1999-141031P 19990625 (60)
 US 1999-143694P 19990714 (60)
 US 1999-151778P 19990831 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 14822
 INCL INCLM: 435/113.000
 INCLS: 435/115.000; 435/252.300
 NCL NCLM: 435/113.000
 NCLS: 435/115.000; 435/252.300
 IC IPCI C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
 C12N0001-20 [I,A]
 IPCR C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];
 C12N0001-20 [I,A]; C12P0013-08 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 10

L5 ANSWER 10 OF 27 USPATFULL on STN
 AN 2006:211028 USPATFULL
 TI Nucleic acid sequences relating to Bacteroides fragilis for diagnostics
 and therapeutics
 IN Breton, Gary L., Marlboro, MA, UNITED STATES
 PA Oscient Pharmaceuticals Corporation, Waltham, MA, UNITED STATES (U.S.
 corporation)
 PI US 7090973 B1 20060815
 AI US 2000-540209 20000404 (9)
 PRAI US 1999-128705P 19990409 (60)
 DT Utility
 FS GRANTED
 LN.CNT 38850
 INCL INCLM: 435/006.000
 INCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330
 NCL NCLM: 435/006.000
 NCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330
 IC IPCI C12Q0001-68 [I,A]; C12P0019-34 [I,A]; C12P0019-00 [I,C*];
 C07H0021-02 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*]
 EXF 435/91.1; 435/91.2; 435/6; 435/320.1; 435/325; 435/352.3; 536/23.1;
 536/24.1; 536/23.7; 536/24.32; 536/24.3; 514/44
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 11-15

L5 ANSWER 11 OF 27 USPATFULL on STN
 AN 2006:146715 USPATFULL
 TI Nucleic acid and amino acid sequences relating to Staphylococcus
 epidermidis for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn, Framingham, MA, UNITED STATES
 Bush, David, Somerville, MA, UNITED STATES
 PA Wyeth, Madison, NJ, UNITED STATES (U.S. corporation)
 PI US 7060458 B1 20060613
 AI US 1999-450969 19991129 (9)
 RLI Continuation-in-part of Ser. No. US 1998-134001, filed on 13 Aug 1998,
 Pat. No. US 6380370, issued on 30 Apr 2002
 PRAI US 1997-64964P 19971108 (60)
 US 1997-55779P 19970814 (60)
 DT Utility
 FS GRANTED
 LN.CNT 35708
 INCL INCLM: 435/069.100

INCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320
 NCL NCLM: 435/069.100
 NCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320
 IC IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C*]
 IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]
 EXF 435/6; 435/91.2; 435/69.1; 536/22.1; 536/23.1; 536/24.3
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 12 OF 27 USPATFULL on STN

AN 2005:299042 USPATFULL

TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF

Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF

Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF

Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF

Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF

PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF

(non-U.S. corporation)

PI US 20050260707 A1 20051124

AI US 2005-55822 A1 20050211 (11)

RLI Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED

PRAI DE 1999-19932125 19990709

DE 1999-19932227 19990709

DE 1999-19932228 19990709

DE 1999-19932230 19990709

DE 1999-19933005 19990714

DE 1999-19933006 19990714

DE 1999-19940764 19990827

DE 1999-19940766 19990827

DE 1999-19940832 19990827

DE 1999-19941378 19990831

DE 1999-19941379 19990831

DE 1999-19942077 19990903

DE 1999-19942079 19990903

DE 1999-19931418 19990708

DE 1999-19932126 19990709

DE 1999-19932229 19990709

DE 1999-19941396 19990831

DE 1999-19942087 19990903

DE 1999-19930476 19990701

DE 1999-19931419 19990708

DE 1999-19931420 19990708

DE 1999-19932206 19990709

DE 1999-19942088 19990903

DE 1999-19942124 19990903

DE 1999-19932928 19990714

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DE 1999-19931443 19990708

DE 1999-19931453 19990708

DE 1999-19931457 19990708

DE 1999-19931465 19990708

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DE 1999-109931541 19990708

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DE 1999-19931632 19990708

DE 1999-19931634 19990708
 DE 1999-19931636 19990708
 DE 1999-19932130 19990708
 DE 1999-19932186 19990709
 DE 1999-19932922 19990714
 DE 1999-19932926 19990714
 DE 1999-19933004 19990714
 DE 1999-19940765 19990827
 DE 1999-19941380 19990831
 DE 1999-19941394 19990831
 DE 1999-19942076 19990903
 DE 1999-19942086 19990903
 DE 1999-19942095 19990903
 DE 1999-19942129 19990903
 US 1999-141031P 19990625 (60)
 US 1999-142101P 19990702 (60)
 US 1999-148613P 19990812 (60)
 US 2000-187970P 20000309 (60)

DT Utility
 FS APPLICATION
 LN.CNT 8777
 INCL INCLM: 435/069.100
 INCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200
 NCL NCLM: 435/069.100
 NCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200
 IC [7]
 ICM C12P021-06
 ICS C12P013-04; C07H021-04; C12N001-20; C12N015-74; C12N009-10
 IPCI C12P0021-06 [ICM,7]; C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C*];
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]; C12N0001-20 [ICS,7];
 C12N0015-74 [ICS,7]; C12N0009-10 [ICS,7]
 IPCR C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
 C07K0014-34 [I,A]; C12N0001-20 [I,C*]; C12N0001-20 [I,A];
 C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];
 C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
 C12P0013-00 [I,C*]; C12P0013-04 [I,A]; C12P0021-06 [I,C*];
 C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 13 OF 27 USPATFULL on STN
 AN 2005:268092 USPATFULL
 TI Modified bacterial surface layer proteins
 IN Pouwels, Pieter Hendrik, Rijswijk, NETHERLANDS
 Smit, Egbert, Sittard, NETHERLANDS
 Tielen, Frans, Prinsenbeek, NETHERLANDS
 PI US 20050233408 A1 20051020
 AI US 2003-500307 A1 20021223 (10)
 WO 2002-EP14749 20021223
 20041122 PCT 371 date

PRAI EP 2001-310937 20011228
 DT Utility
 FS APPLICATION
 LN.CNT 2664
 INCL INCLM: 435/034.000
 INCLS: 530/395.000; 435/252.300
 NCL NCLM: 435/034.000
 NCLS: 435/252.300; 530/395.000
 IC [7]
 ICM C12Q001-04
 ICS C12N001-21; C07K014-335
 IPCI C12Q0001-04 [ICM,7]; C12N0001-21 [ICS,7]; C07K0014-335 [ICS,7];
 C07K0014-195 [ICS,7,C*]

IPCR C12N0015-09 [I,C*]; C12N0015-09 [I,A]; A61K0039-02 [I,C*];
A61K0039-02 [I,A]; A61P0031-00 [I,C*]; A61P0031-04 [I,A];
C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-15 [I,C*];
C12N0001-15 [I,A]; C12N0001-19 [I,C*]; C12N0001-19 [I,A];
C12N0001-20 [I,C*]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
C12N0001-21 [I,A]; C12N0005-10 [I,C*]; C12N0005-10 [I,A];
C12N0015-31 [I,C*]; C12N0015-31 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 14 OF 27 USPATFULL on STN

AN 2005:220997 USPATFULL

TI Corynebacterium glutamicum genes encoding proteins involved in homeostasis and adaptation

IN Pompejus, Markus, Waldsee, GERMANY, FEDERAL REPUBLIC OF
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF

PA Haberbauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF,
D-67056 (non-U.S. corporation)

PI US 20050191732 A1 20050901

AI US 2003-721922 A1 20031124 (10)

RLI Continuation of Ser. No. US 2000-603124, filed on 23 Jun 2000, ABANDONED

PRAI DE 1999-19931418 19990708

DE 1999-19932124 19990709

DE 1999-19932126 19990709

DE 1999-19932127 19990709

DE 1999-19932133 19990709

DE 1999-19932207 19990709

DE 1999-19932208 19990709

DE 1999-19932225 19990709

DE 1999-19932229 19990709

DE 1999-19932914 19990709

DE 1999-19933006 19990709

DE 1999-19940765 19990827

DE 1999-19940768 19990827

DE 1999-19940831 19990827

DE 1999-19940832 19990827

DE 1999-19941385 19990831

DE 1999-19941396 19990831

DE 1999-19942087 19990903

US 1999-141031P 19990625 (60)

US 1999-143694P 19990714 (60)

US 1999-151778P 19990831 (60)

DT Utility

FS APPLICATION

LN.CNT 6552

INCL INCLM: 435/106.000

INCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;

536/023.200

NCL NCLM: 435/106.000

NCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;

536/023.200

IC {7}

ICM C12Q001-68

ICS C07H021-04; C12P013-04; C12N009-10; C12N001-21; C12N015-74

IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];

C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C*]; C12N0009-10 [ICS,7];

C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7]

IPCR C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];

C07K0014-34 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];

C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];

C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
C12P0001-04 [I,C*]; C12P0001-04 [I,A]; C12P0013-00 [I,C*];
C12P0013-04 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 15 OF 27 USPATFULL ON STN
AN 2005:158196 USPATFULL
TI Nucleic acid and amino acid sequences relating to streptococcus
pneumoniae for diagnostics and therapeutics
IN Doucette-Stamm, Lynn A., Framingham, MA, UNITED STATES
Bush, David, Somerville, MA, UNITED STATES
PI US 20050136404 A1 20050623
AI US 2003-617320 A1 20030710 (10)
RLI Division of Ser. No. US 1998-107433, filed on 30 Jun 1998, PENDING
PRAI US 1997-51553P 19970702 (60)
US 1998-85131P 19980512 (60)
DT Utility
FS APPLICATION
LN.CNT 12957
INCL INCLM: 435/006.000
INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700
NCL NCLM: 435/006.000
NCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700
IC [7]
ICM C12Q001-68
ICS C07H021-04; C12N001-21; C07K014-315
IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
C12N0001-21 [ICS,7]; C07K0014-315 [ICS,7]; C07K0014-195
[ICS,7,C*]
IPCR C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
C07K0014-195 [I,C*]; C07K0014-315 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 16-20

L5 ANSWER 16 OF 27 USPATFULL ON STN
AN 2005:131152 USPATFULL
TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface
protein homologues and uses therefore
IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
Alterman, Eric, Apex, NC, UNITED STATES
Buck, B. Logan, Banner Elk, NC, UNITED STATES
Russell, W. Michael, Newburg, IN, UNITED STATES
PI US 20050112612 A1 20050526
US 7348420 B2 20080325
AI US 2004-831070 A1 20040423 (10)
PRAI US 2003-465621P 20030425 (60)
DT Utility
FS APPLICATION
LN.CNT 6100
INCL INCLM: 435/006.000
INCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 530/350.000;
536/023.200
NCL NCLM: 435/023.100; 435/006.000
NCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 530/350.000;
536/023.200
IC [7]
ICM C12Q001-68
ICS C07H021-04; C12P021-06; C12N009-00; C12N001-21; C07K014-335
IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
C12P0021-06 [ICS,7]; C12N0009-00 [ICS,7]; C12N0001-21 [ICS,7];

C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
 IPCI-2 C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12N0001-20 [I,A];
 C12N0015-00 [I,A]; C12P0001-20 [I,A]
 IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
 C07K0014-335 [I,A]; C12N0001-20 [I,C]; C12N0001-20 [I,A];
 C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0009-00 [I,C*];
 C12N0009-00 [I,A]; C12N0015-00 [I,C]; C12N0015-00 [I,A];
 C12P0021-06 [I,C*]; C12P0021-06 [I,A]; C12Q0001-68 [I,C*];
 C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 17 OF 27 USPATFULL on STN
 AN 2004:95339 USPATFULL
 TI Nutritional formulations containing synbiotic substances
 IN Kaup, Susan M., Collingswood, NJ, UNITED STATES
 Wilson, Jeffrey L., Doylestown, PA, UNITED STATES
 Kostek, Beverley M., Glen Mills, PA, UNITED STATES
 Frantz, David C., Pottstown, PA, UNITED STATES
 PA Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)
 PI US 20040072794 A1 20040415
 AI US 2003-681658 A1 20031008 (10)
 PRAI US 2002-418109P 20021011 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 542
 INCL INCLM: 514/054.000
 INCLS: 424/093.450
 NCL NCLM: 514/054.000
 NCLS: 424/093.450
 IC [7]
 ICM A61K045-00
 ICS A61K031-715
 IPCI A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]
 IPCR A23L0001-052 [I,C*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C*];
 A23L0001-29 [I,A]; A23L0001-30 [I,C*]; A23L0001-30 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 18 OF 27 USPATFULL on STN
 AN 2004:12970 USPATFULL
 TI Polynucleotides, materials incorporating them, and methods for using them
 IN Glenn, Matthew, Whenuapai, NEW ZEALAND
 Havukkala, Ilkka J., Remuera, NEW ZEALAND
 Lubbers, Mark, Palmerston North, NEW ZEALAND
 Dekker, James, Palmerston North, NEW ZEALAND
 PA GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND
 (non-U.S. corporation)
 PI US 20040009490 A1 20040115
 US 7125698 B2 20061024
 AI US 2002-264213 A1 20021003 (10)
 RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,
 PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug
 2000, GRANTED, Pat. No. US 6544772
 PRAI US 1999-147853P 19990809 (60)
 US 1999-147852P 19990809 (60)
 US 1999-152032P 19990901 (60)
 US 1999-152031P 19990901 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 5375
 INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200

NCL NCLM: 435/193.000; 435/006.000
 NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;
 435/252.300; 435/320.100; 536/023.200

IC [7]
 ICM C12Q001-68
 ICS C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335
 IPCI C12Q0001-68 [ICM,7]; C07H0021-00 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];
 C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
 IPCI-2 C12N0009-10 [I,A]
 IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C*];
 A23C0019-032 [I,A]; A61K0038-00 [N,C*]; A61K0038-00 [N,A];
 C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 19 OF 27 USPATFULL on STN
 AN 2004:250212 USPATFULL
 TI Nucleic acid and amino acid sequences relating to Streptococcus
 pneumoniae for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn A., Framingham, MA, United States
 Bush, David, Somerville, MA, United States
 PA Genome Therapeutics Corporation, Waltham, MA, United States (U.S.
 corporation)
 PI US 6800744 B1 20041005
 AI US 1998-107433 19980630 (9)
 PRAI US 1998-85131P 19980512 (60)
 US 1997-51553P 19970702 (60)
 DT Utility
 FS GRANTED
 LN.CNT 11545
 INCL INCLM: 536/023.100
 INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;
 536/024.100; 536/023.400; 536/024.320

NCL NCLM: 536/023.100
 NCLS: 435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;
 536/024.100; 536/024.320

IC [7]
 ICM C12Q001-68
 ICS C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;
 C07H021-04
 IPCI C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];
 C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
 IPCR C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
 C07K0014-195 [I,C*]; C07K0014-315 [I,A]
 EXF 536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;
 435/6

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 20 OF 27 USPATFULL on STN
 AN 2003:71519 USPATFULL
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF
 Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF
 Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF
 PI US 20030049804 A1 20030313

AI US 2000-746660 A1 20001222 (9)
 RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
 PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
 2000, PENDING
 PRAI DE 1999-19931420 19990708
 US 1999-141031P 19990625 (60)
 US 1999-142101P 19990702 (60)
 US 1999-148613P 19990812 (60)
 US 2000-187970P 20000309 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 15004
 INCL INCLM: 435/115.000
 INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200
 NCL NCLM: 435/115.000
 NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200
 IC [7]
 ICM C12P013-08
 ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21
 IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
 C07H0021-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];
 C12N0001-21 [ICS,7]
 IPCR C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
 C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];
 C12N0009-90 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 17

L5 ANSWER 17 OF 27 USPATFULL on STN
 AN 2004:95339 USPATFULL
 TI Nutritional formulations containing synbiotic substances
 IN Kaup, Susan M., Collingswood, NJ, UNITED STATES
 Wilson, Jeffrey L., Doylestown, PA, UNITED STATES
 Kostek, Beverley M., Glen Mills, PA, UNITED STATES
 Frantz, David C., Pottstown, PA, UNITED STATES
 PA Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)
 PI US 20040072794 A1 20040415
 AI US 2003-681658 A1 20031008 (10)
 PRAI US 2002-418109P 20021011 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 542
 INCL INCLM: 514/054.000
 INCLS: 424/093.450
 NCL NCLM: 514/054.000
 NCLS: 424/093.450
 IC [7]
 ICM A61K045-00
 ICS A61K031-715
 IPCI A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]
 IPCR A23L0001-052 [I,C*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C*];
 A23L0001-29 [I,A]; A23L0001-30 [I,C*]; A23L0001-30 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 17 ab

L5 ANSWER 17 OF 27 USPATFULL on STN
 AB Nutritional compositions are provided which comprise oligofructose,

sialyllactose and probiotic bacteria, which are useful in the eradication of pathogenic microorganisms in the gastrointestinal tracts of patients.

=> d 15 17 kwic

L5 ANSWER 17 OF 27 USPATFULL on STN

SUMM [0004] Prebiotics are nondigestible food ingredients that that beneficially affect the host by selectively stimulating the growth and/or activity of one or a limited number. . .

SUMM [0011] Sialyllactose is known to have anti-adhesive properties for specific pathogenic bacteria. For example, sialyllactose acts to inhibit cholera toxin invitro (Idota et al., "Inhibition of Cholera Toxin by Human Milk Fractions and Sialyllactose," Biosci. Biotech. Biochem. 59:417-419) and Helicobacter pylori (Simon et al., "Inhibition of Helicobacter pylori Binding to Gastrointestinal Epithelial Cells by Sialic Acid-Containing Oligosaccharides," Infection and Immunity, 750-757, (1997)).

SUMM [0015] Probiotics are live microbial food ingredients that have a beneficial effect on human health. (Salminen et al., "Functional food science and gastrointestinal physiology and function." Brit. J. Nutr. 80(suppl. 1):S147-S171 (1998)).

SUMM . . . carbohydrate to lactic acid. The specific strains most often studied include members of the genera Lactobacillus and Bifidobacterium. (Sanders, "Probiotics." Food Technol. 53:67-77 (1999)).

SUMM [0017] Some lactic acid bacteria specifically produce lactic acid as a major product of their metabolism. Some produce predominantly the levorotary "L"-form of lactic acid [L(+)-lactic acid], others produce predominantly the dextrorotary "D"-form. . .

SUMM [0019] A milk product containing LGG significantly shortened the duration of diarrhea in young children. (Kaila et al., "Enhancement of the circulating antibody secreting. . .

SUMM [0021] U.S. Pat. No. 5,908,646 discloses a method for inhibiting the growth or activity of Clostridium species in a human food product by adding an effective amount of the beneficial microorganism, L. rhamnosus [L. casei subspecies rhamnosus], which produces predominantly L(+)-lactic acid.

SUMM . . . viable cells of three specific microorganisms beneficial to the human intestinal microorganisms for preventing diarrhea. Specifically, the three microorganisms are Lactobacillus reuteri, Lactobacillus acidophilus and Bifidobacterium infantis. The diarrhea can be caused by antibiotic treatment or by infection with a virus, a. . .

SUMM . . . "Bifidobacterium bifidum." (Fukushima et al., "Effect of a probiotic formula on intestinal immunoglobulin A production in healthy children." Int. J. Food Microb. 42-39-44 (1998)).

=> d 15 18

L5 ANSWER 18 OF 27 USPATFULL on STN

AN 2004:12970 USPATFULL

TI Polynucleotides, materials incorporating them, and methods for using them

IN Glenn, Matthew, Whenuapai, NEW ZEALAND
Havukkala, Ilkka J., Remuera, NEW ZEALAND
Lubbers, Mark, Palmerston North, NEW ZEALAND
Dekker, James, Palmerston North, NEW ZEALAND

PA GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND
(non-U.S. corporation)

PI US 20040009490 A1 20040115
US 7125698 B2 20061024

AI US 2002-264213 AI 20021003 (10)
 RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,
 PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug
 2000, GRANTED, Pat. No. US 6544772
 PRAI US 1999-147853P 19990809 (60)
 US 1999-147852P 19990809 (60)
 US 1999-152032P 19990901 (60)
 US 1999-152031P 19990901 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 5375
 INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200
 NCL NCLM: 435/193.000; 435/006.000
 NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;
 435/252.300; 435/320.100; 536/023.200
 IC [7]
 ICM C12Q001-68
 ICS C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];
 C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
 IPCI-2 C12N0009-10 [I,A]
 IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C*];
 A23C0019-032 [I,A]; A61K0038-00 [N,C*]; A61K0038-00 [N,A];
 C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 19

L5 ANSWER 19 OF 27 USPATFULL ON STN
 AN 2004:250212 USPATFULL
 TI Nucleic acid and amino acid sequences relating to Streptococcus
 pneumoniae for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn A., Framingham, MA, United States
 Bush, David, Somerville, MA, United States
 PA Genome Therapeutics Corporation, Waltham, MA, United States (U.S.
 corporation)
 PI US 6800744 B1 20041005
 AI US 1998-107433 19980630 (9)
 PRAI US 1998-85131P 19980512 (60)
 US 1997-51553P 19970702 (60)
 DT Utility
 FS GRANTED
 LN.CNT 11545
 INCL INCLM: 536/023.100
 INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;
 536/024.100; 536/023.400; 536/024.320
 NCL NCLM: 536/023.100
 NCLS: 435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;
 536/024.100; 536/024.320
 IC [7]
 ICM C12Q001-68
 ICS C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;
 C07H021-04
 IPCI C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];
 C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
 IPCR C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
 C07K0014-195 [I,C*]; C07K0014-315 [I,A]

EXF 536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;
435/6

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 20-28

L5 ANSWER 20 OF 27 USPATFULL on STN

AN 2003:71519 USPATFULL

TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF

Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF

Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF

Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF

Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF

Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF

Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF

Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF

PI US 20030049804 A1 20030313

AI US 2000-746660 A1 20001222 (9)

RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
2000, PENDING

PRAI DE 1999-19931420 19990708

US 1999-141031P 19990625 (60)

US 1999-142101P 19990702 (60)

US 1999-148613P 19990812 (60)

US 2000-187970P 20000309 (60)

DT Utility

FS APPLICATION

LN.CNT 15004

INCL INCLM: 435/115.000

INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200

NCL NCLM: 435/115.000

NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200

IC [7]

ICM C12P013-08

ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21

IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];

C07H0021-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];

C12N0001-21 [ICS,7]

IPCR C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];

C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];

C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];

C12N0009-90 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 21 OF 27 USPATFULL on STN

AN 2003:95966 USPATFULL

TI Polynucleotides, materials incorporating them, and methods for using
them

IN Glenn, Matthew, Auckland, NEW ZEALAND

Havukkala, Ilkka J., Auckland, NEW ZEALAND

Bloksberg, Leonard N., Auckland, NEW ZEALAND

Lubbers, Mark W., Palmerston North, NEW ZEALAND

Dekker, James, Palmerston North, NEW ZEALAND

Christensson, Anna C., Lund, SWEDEN

Holland, Ross, Palmerston North, NEW ZEALAND

O'Toole, Paul W., Palmerston North, NEW ZEALAND

Reid, Julian R., Palmerston North, NEW ZEALAND

Coolbear, Timothy, Palmerston North, NEW ZEALAND

PA Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.)

corporation)
Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.
corporation)
PI US 6544772 B1 20030408
AI US 2000-634238 20000808 (9)
DT Utility
FS GRANTED
LN.CNT 2015
INCL INCLM: 435/252.300
INCLS: 435/320.100; 536/023.700
NCL NCLM: 435/252.300
NCLS: 435/320.100; 536/023.700
IC [7]
ICM C12N001-21
ICS C12N015-63; C12N015-31
IPCI C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]
IPCR A23C0019-00 [I,C*]; A23C0019-032 [I,A]; C07K0014-195 [I,C*];
C07K0014-335 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
C12N0015-31 [I,C*]; C12N0015-31 [I,A]
EXF 435/252.3; 435/320.1; 536/23.7
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 22 OF 27 BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS ON STN
AN 1999-00562 BIOTECHDS
TI Use of lactic and propionic acid bacteria;
to bind mycotoxin to prevent their absorption or to purify
contaminated food or feedstuff
AU El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J
PA Roy.Melbourne-Inst.Technol.
LO Melbourne, Victoria, Australia.
PI WO 9834503 13 Aug 1998
AI WO 1998-AU63 6 Feb 1998
PRAI AU 1997-5005 7 Feb 1997
DT Patent
LA English
OS WPI: 1998-557001 [49]

L5 ANSWER 23 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): CP000705 GenBank (R)
GenBank ACC. NO. (GBN): CP000705 AAOV01000000 AAOV01000001-AAOV01000097
GenBank VERSION (VER): CP000705.1 GI:148530277
SEQUENCE LENGTH (SQL): 1999618
MOLECULE TYPE (CI): DNA; circular
DIVISION CODE (CI): Bacteria
DATE (DATE): 17 Oct 2007
DEFINITION (DEF): Lactobacillus reuteri F275,
complete genome.
SOURCE: Lactobacillus reuteri F275
ORGANISM (ORGN): Lactobacillus reuteri F275
Bacteria; Firmicutes; Lactobacillales;
Lactobacillaceae; Lactobacillus
PROJECT (PJID): GenomeProject:15766
COMMENT:
URL -- <http://www.jgi.doe.gov>
JGI Project ID: 4000135
Source DNA available from Gerald Tannock
(gerald.tannock@stonebow.otago.ac.nz)
Bacteria available from DSMZ: DSM 20016
Contacts: Gerald Tannock (gerald.tannock@stonebow.otago.ac.nz)
Paul Richardson (microbes@cuba.jgi-psf.org)
Quality assurance done by JGI-Stanford

Annotation done by JGI-ORNL and JGI-PGF

Finishing done by JGI-PGF

Finished microbial genomes have been curated to close all gaps with greater than 98% coverage of at least two independent clones. Each base pair has a minimum q (quality) value of 30 and the total error rate is less than one per 50000.

The JGI and collaborators endorse the principles for the distribution and use of large scale sequencing data adopted by the larger genome sequencing community and urge users of this data to follow them. It is our intention to publish the work of this project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.cfm?pageID=10506376>).

REFERENCE: 1 (bases 1 to 1999618)

AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.

TITLE (TI): Complete sequence of chromosome of
Lactobacillus reuteri DSM 20016

JOURNAL (SO): Unpublished

REFERENCE: 2 (bases 1 to 1999618)

AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (17-MAY-2007) US DOE Joint Genome Institute,
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698,
USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1999618	/organism="Lactobacillus reuteri F275" /mol-type="genomic DNA" /strain="DSM 20016" /db-xref="taxon:299033" /note="F275 = DSM 20016 = JCM 1112"

L5 ANSWER 24 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM270397 GenBank (R)

GenBank ACC. NO. (GBN): AM270397

GenBank VERSION (VER): AM270397.1 GI:134084136

CAS REGISTRY NO. (RN): 928607-03-8

SEQUENCE LENGTH (SQL): 163680

MOLECULE TYPE (CI): DNA; linear

DIVISION CODE (CI): Plants, fungi, algae

DATE (DATE): 24 Mar 2007

DEFINITION (DEF): Aspergillus niger contig An18c0040, complete genome.

SOURCE: Aspergillus niger

ORGANISM (ORGN): Aspergillus niger

Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic
Trichocomaceae; Aspergillus

REFERENCE: 1 (bases 150631 to 153085)

AUTHOR (AU): Habison,A.; Kubicek,C.P.; Rohr,M.
 TITLE (TI): Partial purification and regulatory properties of phosphofructokinase from *Aspergillus niger*
 JOURNAL (SO): Biochem. J., 209 (3), 669-676 (1983)
 OTHER SOURCE (OS): CA 99:171737
 REFERENCE: 2 (bases 71863 to 73356)
 AUTHOR (AU): Manney,T.R.
 TITLE (TI): Expression of the BAR1 gene in *Saccharomyces cerevisiae*: induction by the alpha mating pheromone of an activity associated with a secreted protein
 JOURNAL (SO): J. Bacteriol., 155 (1), 291-301 (1983)
 OTHER SOURCE (OS): CA 99:102121
 REFERENCE: 3 (bases 71863 to 73356)
 AUTHOR (AU): Jones,E.W.
 TITLE (TI): The synthesis and function of proteases in *Saccharomyces*: genetic approaches
 JOURNAL (SO): Annu. Rev. Genet., 18, 233-270 (1984)
 OTHER SOURCE (OS): CA 102:92538
 REFERENCE: 4 (bases 144032 to 145578)
 AUTHOR (AU): Brandsch,R.; Bichler,V.
 TITLE (TI): In vivo and in vitro expression of the 6-hydroxy-D-nicotine oxidase gene of *Arthrobacter oxidans*, cloned into *Escherichia coli*, as an enzymatically active, covalently flavinylated polypeptide
 JOURNAL (SO): FEBS Lett., 192 (2), 204-208 (1985)
 OTHER SOURCE (OS): CA 104:29597
 REFERENCE: 5 (bases 150631 to 153085)
 AUTHOR (AU): Schreiferl,G.; Kubicek,C.P.; Rohr,M.
 TITLE (TI): Inhibition of citric acid accumulation by manganese ions in *Aspergillus niger* mutants with reduced citrate control of phosphofructokinase
 JOURNAL (SO): J. Bacteriol., 165 (3), 1019-1022 (1986)
 OTHER SOURCE (OS): CA 104:165023
 REFERENCE: 6 (bases 156827 to 158638)
 AUTHOR (AU): Whittington,H.A.; Grant,S.; Roberts,C.F.; Lamb,H.; Hawkins,A.R.
 TITLE (TI): Identification and isolation of a putative permease gene in the quinic acid utilization (QUT) gene cluster of *Aspergillus nidulans*
 JOURNAL (SO): Curr. Genet., 12 (2), 135-139 (1987)
 OTHER SOURCE (OS): CA 107:91128
 REFERENCE: 7 (bases 54105 to 55762)
 AUTHOR (AU): Chisholm,V.T.; Lea,H.Z.; Rai,R.; Cooper,T.G.
 TITLE (TI): Regulation of allantoin transport in wild-type and mutant strains of *Saccharomyces cerevisiae*
 JOURNAL (SO): J. Bacteriol., 169 (4), 1684-1690 (1987)
 OTHER SOURCE (OS): CA 106:172689
 REFERENCE: 8 (bases 71863 to 73356)
 AUTHOR (AU): MacKay,V.L.; Welch,S.K.; Insley,M.Y.; Manney,T.R.; Holly,J.; Saari,G.C.; Parker,M.L.
 TITLE (TI): The *Saccharomyces cerevisiae* BAR1 gene encodes an exported protein with homology to pepsin
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 85 (1), 55-59 (1988)
 OTHER SOURCE (OS): CA 108:125658
 REFERENCE: 9 (bases 54105 to 55762)
 AUTHOR (AU): Rai,R.; Genbauffe,F.S.; Cooper,T.G.
 TITLE (TI): Structure and transcription of the allantoin permease gene (DAL5) from *Saccharomyces cerevisiae*
 JOURNAL (SO): J. Bacteriol., 170 (1), 266-271 (1988)
 OTHER SOURCE (OS): CA 109:17930
 REFERENCE: 10

AUTHOR (AU): Hawkins,A.R.; Lamb,H.K.; Smith,M.; Keyte,J.W.;
 Roberts,C.F.

TITLE (TI): Molecular organisation of the quinic acid utilization
 (QUT) gene cluster in *Aspergillus nidulans*

JOURNAL (SO): Mol. Gen. Genet., 214 (2), 224-231 (1988)

OTHER SOURCE (OS): CA 111:188522

REFERENCE: 11 (bases 68231 to 69040)

AUTHOR (AU): Honjo,M.; Nakayama,A.; Fukazawa,K.; Kawamura,K.;
 Ando,K.; Furutani,Y.

TITLE (TI): A novel *Bacillus subtilis* gene involved in negative
 control of sporulation and degradative-enzyme
 production

JOURNAL (SO): J. Bacteriol., 172 (4), 1783-1790 (1990)

OTHER SOURCE (OS): CA 113:146166

REFERENCE: 12 (bases 5212 to 7379)

AUTHOR (AU): Nikawa,J.; Hosaka,K.; Tsukagoshi,Y.; Yamashita,S.

TITLE (TI): Primary structure of the yeast choline transport gene
 and regulation of its expression

JOURNAL (SO): J. Biol. Chem., 265 (26), 15996-16003 (1990)

OTHER SOURCE (OS): CA 114:18549

REFERENCE: 13 (bases 159975 to 161849)

AUTHOR (AU): Fling,M.E.; Kopf,J.; Tamarkin,A.; Gorman,J.A.;
 Smith,H.A.; Koltin,Y.

TITLE (TI): Analysis of a *Candida albicans* gene that encodes a
 novel mechanism for resistance to benomyl and
 methotrexate

JOURNAL (SO): Mol. Gen. Genet., 227 (2), 318-329 (1991)

OTHER SOURCE (OS): CA 116:100405

REFERENCE: 14 (bases 28874 to 30837)

AUTHOR (AU): Masuda,N.; Kitamura,N.; Saito,K.

TITLE (TI): Primary structure of protein moiety of *Penicillium*
notatum phospholipase B deduced from the cDNA

JOURNAL (SO): Eur. J. Biochem., 202 (3), 783-787 (1991)

OTHER SOURCE (OS): CA 118:76020

REFERENCE: 15 (bases 100363 to 101496)

AUTHOR (AU): Sakoda,H.; Imanaka,T.

TITLE (TI): Cloning and sequencing of the gene coding for alcohol
 dehydrogenase of *Bacillus stearothermophilus* and
 rational shift of the optimum pH

JOURNAL (SO): J. Bacteriol., 174 (4), 1397-1402 (1992)

OTHER SOURCE (OS): CA 118:186708

REFERENCE: 16 (bases 20773 to 22555)

AUTHOR (AU): Kamoda,S.; Saburi,Y.

TITLE (TI): Structural and enzymatical comparison of
 lignostilbene- α , β -dioxygenase isozymes, I, II,
 and III, from *Pseudomonas paucimobilis* TMY1009

JOURNAL (SO): Biosci. Biotechnol. Biochem., 57 (6), 931-934 (1993)

OTHER SOURCE (OS): CA 119:154577

REFERENCE: 17 (bases 80602 to 83154)

AUTHOR (AU): ElBerry,H.M.; Majumdar,M.L.; Cunningham,T.S.;
 Sumrada,R.A.; Cooper,T.G.

TITLE (TI): Regulation of the urea active transporter gene (DUR3)
 in *Saccharomyces cerevisiae*

JOURNAL (SO): J. Bacteriol., 175 (15), 4688-4698 (1993)

OTHER SOURCE (OS): CA 119:242524

REFERENCE: 18 (bases 23096 to 24052)

AUTHOR (AU): Roper,D.I.; Cooper,R.A.

TITLE (TI): Purification, nucleotide sequence and some properties
 of a bifunctional isomerase/decarboxylase from the
 homoprotocatechuate degradative pathway of *Escherichia*
coli C

JOURNAL (SO): Eur. J. Biochem., 217 (2), 575-580 (1993)

OTHER SOURCE (OS): CA 119:265270
REFERENCE: 19 (bases 5212 to 7379)
AUTHOR (AU): Li,Z.; Brendel,M.
TITLE (TI): Co-regulation with genes of phospholipid biosynthesis of the CTR/HNMI-encoded choline/nitrogen mustard permease in *Saccharomyces cerevisiae*
Mol. Gen. Genet., 241 (5-6), 680-684 (1993)
JOURNAL (SO):
OTHER SOURCE (OS): CA 121:28475
REFERENCE: 20 (bases 159975 to 161849)
AUTHOR (AU): Ben-Yaacov,R.; Knoller,S.; Caldwell,G.A.; Becker,J.M.; Koltin,Y.
TITLE (TI): *Candida albicans* gene encoding resistance to benomyl and methotrexate is a multidrug resistance gene
JOURNAL (SO): Antimicrob. Agents Chemother., 38 (4), 648-652 (1994)
OTHER SOURCE (OS): CA 121:2236
REFERENCE: 21 (bases 150631 to 153085)
AUTHOR (AU): Legisa,M.; Bencina,M.
TITLE (TI): Evidence for the activation of 6-phosphofructo-1-kinase by cAMP-dependent protein kinase in *Aspergillus niger*
JOURNAL (SO): FEMS Microbiol. Lett., 118 (3), 327-333 (1994)
OTHER SOURCE (OS): CA 121:102759
REFERENCE: 22 (bases 138020 to 140061)
AUTHOR (AU): Kim,Y.J.; Bjorklund,S.; Li,Y.; Sayre,M.H.; Kornberg,R.D.
TITLE (TI): A multiprotein mediator of transcriptional activation and its interaction with the C-terminal repeat domain of RNA polymerase II
JOURNAL (SO): Cell, 77 (4), 599-608 (1994)
OTHER SOURCE (OS): CA 121:102149
REFERENCE: 23 (bases 38805 to 39836)
AUTHOR (AU): Downs,D.M.; Petersen,L.
TITLE (TI): *apbA*, a new genetic locus involved in thiamine biosynthesis in *Salmonella typhimurium*
JOURNAL (SO): J. Bacteriol., 176 (16), 4858-4864 (1994)
OTHER SOURCE (OS): CA 121:197350
REFERENCE: 24 (bases 5212 to 7379)
AUTHOR (AU): Li,Z.; Brendel,M.
TITLE (TI): Sensitivity to nitrogen mustard in *Saccharomyces cerevisiae* is independently determined by regulated choline permease and DNA repair
JOURNAL (SO): Mutat. Res., 315 (2), 139-145 (1994)
OTHER SOURCE (OS): CA 121:198201
REFERENCE: 25 (bases 85096 to 90863)
AUTHOR (AU): Szczypka,M.S.; Wemmie,J.A.; Moye-Rowley,W.S.; Thiele,D.J.
TITLE (TI): A yeast metal resistance protein similar to human cystic fibrosis transmembrane conductance regulator (CFTR) and multidrug resistance-associated protein
JOURNAL (SO): J. Biol. Chem., 269 (36), 22853-22857 (1994)
OTHER SOURCE (OS): CA 122:26140
REFERENCE: 26 (bases 91484 to 93088)
AUTHOR (AU): Knight,S.A.; Tamai,K.T.; Kosman,D.J.; Thiele,D.J.
TITLE (TI): Identification and analysis of a *Saccharomyces cerevisiae* copper homeostasis gene encoding a homeodomain protein
JOURNAL (SO): Mol. Cell. Biol., 14 (12), 7792-7804 (1994)
OTHER SOURCE (OS): CA 122:73697
REFERENCE: 27 (bases 85096 to 90863)
AUTHOR (AU): Wemmie,J.A.; Szczypka,M.S.; Thiele,D.J.; Moye-Rowley,W.S.
TITLE (TI): Cadmium tolerance mediated by the yeast AP-1 protein requires the presence of an ATP-binding cassette

transporter-encoding gene, YCF1

JOURNAL (SO): J. Biol. Chem., 269 (51), 32592-32597 (1994)

OTHER SOURCE (OS): CA 121:294343

REFERENCE: 28 (bases 20773 to 22555)

AUTHOR (AU): Kamoda, S.; Saburi, Y.

TITLE (TI): Cloning of a lignostilbene- α , β -dioxygenase isozyme gene from *Pseudomonas paucimobilis* TMY1009

JOURNAL (SO): Biosci. Biotechnol. Biochem., 59 (10), 1866-1868 (1995)

OTHER SOURCE (OS): CA 124:47043

REFERENCE: 29 (bases 85096 to 90863)

AUTHOR (AU): Li, Z.S.; Szczypka, M.; Lu, Y.P.; Thiele, D.J.; Rea, P.A.

TITLE (TI): The yeast cadmium factor protein (YCF1) is a vacuolar glutathione S-conjugate pump

JOURNAL (SO): J. Biol. Chem., 271 (11), 6509-6517 (1996)

OTHER SOURCE (OS): CA 124:226108

REFERENCE: 30 (bases 33419 to 35477)

AUTHOR (AU): Silva, J.C.; Minto, R.E.; Barry, C.E. III; Holland, K.A.; Townsend, C.A.

TITLE (TI): Isolation and characterization of the versicolorin B synthase gene from *Aspergillus parasiticus*. Expansion of the aflatoxin B1 biosynthetic gene cluster

JOURNAL (SO): J. Biol. Chem., 271 (23), 13600-13608 (1996)

OTHER SOURCE (OS): CA 125:50401

REFERENCE: 31 (bases 15614 to 17392)

AUTHOR (AU): Covert, S.F.; Enkerli, J.; Miao, V.P.; VanEtten, H.D.

TITLE (TI): A gene for maackiain detoxification from a dispensable chromosome of *Nectria haematococca*

JOURNAL (SO): Mol. Gen. Genet., 251 (4), 397-406 (1996)

OTHER SOURCE (OS): CA 125:106677

REFERENCE: 32 (bases 131646 to 132375)

AUTHOR (AU): Mitsuhashi, S.; Miyachi, S.

TITLE (TI): Amino acid sequence homology between N- and C-terminal halves of a carbonic anhydrase in *Porphyridium purpureum*, as deduced from the cloned cDNA

JOURNAL (SO): J. Biol. Chem., 271 (45), 28703-28709 (1996)

OTHER SOURCE (OS): CA 125:321312

REFERENCE: 33 (bases 85096 to 90863)

AUTHOR (AU): Li, Z.S.; Lu, Y.P.; Zhen, R.G.; Szczypka, M.; Thiele, D.J.; Rea, P.A.

TITLE (TI): A new pathway for vacuolar cadmium sequestration in *Saccharomyces cerevisiae*: YCF1-catalyzed transport of bis(glutathionato)cadmium

JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 94 (1), 42-47 (1997)

OTHER SOURCE (OS): CA 126:127966

REFERENCE: 34 (bases 1241 to 3043)

AUTHOR (AU): Saito, Y.; Ishii, Y.; Hayashi, H.; Imao, Y.; Akashi, T.; Yoshikawa, K.; Noguchi, Y.; Soeda, S.; Yoshida, M.; Niwa, M.; Hosoda, J.; Shimomura, K.

TITLE (TI): Cloning of genes coding for L-sorbose and L-sorbose dehydrogenases from *Gluconobacter oxydans* and microbial production of 2-keto-L-gulonate, a precursor of L-ascorbic acid, in a recombinant *G. oxydans* strain

JOURNAL (SO): Appl. Environ. Microbiol., 63 (2), 454-460 (1997)

OTHER SOURCE (OS): CA 126:167180

REFERENCE: 35 (bases 150631 to 153085)

AUTHOR (AU): Ruijter, G.J.; Panneman, H.; Visser, J.

TITLE (TI): Overexpression of phosphofructokinase and pyruvate kinase in citric acid-producing *Aspergillus niger*

JOURNAL (SO): Biochim. Biophys. Acta, 1334 (2-3), 317-326 (1997)

OTHER SOURCE (OS): CA 126:222695

REFERENCE: 36 (bases 49850 to 51919)

AUTHOR (AU): Prieto, R.; Woloshuk, C.P.

TITLE (TI): ordi, an oxidoreductase gene responsible for conversion of O-methylsterigmatocystin to aflatoxin in *Aspergillus flavus*

JOURNAL (SO): Appl. Environ. Microbiol., 63 (5), 1661-1666 (1997)

OTHER SOURCE (OS): CA 127:13942

REFERENCE: 37 (bases 17766 to 20491)

AUTHOR (AU): Todd, R.B.; Murphy, R.L.; Martin, H.M.; Sharp, J.A.; Davis, M.A.; Katz, M.E.; Hynes, M.J.

TITLE (TI): The acetate regulatory gene *facB* of *Aspergillus nidulans* encodes a Zn(II)2Cys6 transcriptional activator

JOURNAL (SO): Mol. Gen. Genet., 254 (5), 495-504 (1997)

OTHER SOURCE (OS): CA 127:105007

REFERENCE: 38 (bases 71863 to 73356)

AUTHOR (AU): Ballensiefen, W.; Schmitt, H.D.

TITLE (TI): Periplasmic Barl protease of *Saccharomyces cerevisiae* is active before reaching its extracellular destination

JOURNAL (SO): Eur. J. Biochem., 247 (1), 142-147 (1997)

OTHER SOURCE (OS): CA 127:187926

REFERENCE: 39 (bases 52148 to 53720)

AUTHOR (AU): Kuroyanagi, N.; Onogi, H.; Wakabayashi, T.; Hagiwara, M.

TITLE (TI): Novel SR-protein-specific kinase, SRPK2, disassembles nuclear speckles

JOURNAL (SO): Biochem. Biophys. Res. Commun., 242 (2), 357-364 (1998)

OTHER SOURCE (OS): CA 128:241040

REFERENCE: 40 (bases 113565 to 114733)

AUTHOR (AU): MacDiarmid, C.W.; Gardner, R.C.

TITLE (TI): Overexpression of the *Saccharomyces cerevisiae* magnesium transport system confers resistance to aluminum ion

JOURNAL (SO): J. Biol. Chem., 273 (3), 1727-1732 (1998)

OTHER SOURCE (OS): CA 128:177021

REFERENCE: 41 (bases 135940 to 137166)

AUTHOR (AU): Wang, H.Y.; Lin, W.; Dyck, J.A.; Yeakley, J.M.; Songyang, Z.; Cantley, L.C.; Fu, X.D.

TITLE (TI): SRPK2: a differentially expressed SR protein-specific kinase involved in mediating the interaction and localization of pre-mRNA splicing factors in mammalian cells

JOURNAL (SO): J. Cell Biol., 140 (4), 737-750 (1998)

OTHER SOURCE (OS): CA 128:306636

REFERENCE: 42 (bases 38805 to 39836)

AUTHOR (AU): Prody, M.E.; Downs, D.

TITLE (TI): AppA, the ketopantoate reductase enzyme of *Salmonella typhimurium* is required for the synthesis of thiamine via the alternative pyrimidine biosynthetic pathway

JOURNAL (SO): J. Biol. Chem., 273 (10), 5572-5576 (1998)

OTHER SOURCE (OS): CA 128:305459

REFERENCE: 43 (bases 106231 to 106803)

AUTHOR (AU): Woloshuk, C.P.; Prieto, R.

TITLE (TI): Genetic organization and function of the aflatoxin B1 biosynthetic genes

JOURNAL (SO): FEMS Microbiol. Lett., 160 (2), 169-176 (1998)

OTHER SOURCE (OS): CA 128:290649

REFERENCE: 44 (bases 93571 to 94963)

AUTHOR (AU): Philp, N.J.; Yoon, H.; Grollman, E.F.

TITLE (TI): Monocarboxylate transporter MCT1 is located in the apical membrane and MCT3 in the basal membrane of rat RPE

JOURNAL (SO): Am. J. Physiol., 274 (6 Pt 2), R1824-R1828 (1998)

OTHER SOURCE (OS): CA 129:159493

REFERENCE: 45 (bases 93571 to 94963)

AUTHOR (AU): Wilson, M.C.; Jackson, V.N.; Heddle, C.; Price, N.T.; Pilegaard, H.; Juel, C.; Bonen, A.; Montgomery, I.; Hutter, O.F.; Halestrap, A.P.

TITLE (TI): Lactic acid efflux from white skeletal muscle is catalyzed by the monocarboxylate transporter isoform MCT3

JOURNAL (SO): J. Biol. Chem., 273 (26), 15920-15926 (1998)

OTHER SOURCE (OS): CA 129:159801

REFERENCE: 46 (bases 153410 to 154508)

AUTHOR (AU): Dekkers, L.C.; van der Bij, A.J.; Mulders, I.H.; Phoelich, C.C.; Wentwoord, R.A.; Glandorf, D.C.; Wijffelman, C.A.; Lugtenberg, B.J.

TITLE (TI): Role of the O-antigen of lipopolysaccharide, and possible roles of growth rate and of NADH:ubiquinone oxidoreductase (nuo) in competitive tomato root-tip colonization by *Pseudomonas fluorescens* WCS365

JOURNAL (SO): Mol. Plant Microbe Interact., 11 (8), 763-771 (1998)

OTHER SOURCE (OS): CA 129:200426

REFERENCE: 47 (bases 146433 to 148685)

AUTHOR (AU): Saito, K.; Yamazaki, H.; Ohnishi, Y.; Fujimoto, S.; Takahashi, E.; Horinouchi, S.

TITLE (TI): Production of trehalose synthase from a basidiomycete, *Grifola frondosa*, in *Escherichia coli*

JOURNAL (SO): Appl. Microbiol. Biotechnol., 50 (2), 193-198 (1998)

OTHER SOURCE (OS): CA 130:956

REFERENCE: 48 (bases 122486 to 123895)

AUTHOR (AU): Kimura, M.; Matsumoto, G.; Shingu, Y.; Yoneyama, K.; Yamaguchi, I.

TITLE (TI): The mystery of the trichothecene 3-O-acetyltransferase gene. Analysis of the region around Tri101 and characterization of its homologue from *Fusarium sporotrichioides*

JOURNAL (SO): FEBS Lett., 435 (2-3), 163-168 (1998)

OTHER SOURCE (OS): CA 130:11163

REFERENCE: 49 (bases 146433 to 148685)

AUTHOR (AU): Saito, K.; Kase, T.; Takahashi, E.; Horinouchi, S.

TITLE (TI): Purification and characterization of a trehalose synthase from the basidiomycete *grifola frondosa*

JOURNAL (SO): Appl. Environ. Microbiol., 64 (11), 4340-4345 (1998)

OTHER SOURCE (OS): CA 130:34870

REFERENCE: 50 (bases 14029 to 15172)

AUTHOR (AU): Feng, Y.; Khoo, H.E.; Poh, C.L.

TITLE (TI): Purification and characterization of gentisate 1,2-dioxygenases from *Pseudomonas alcaligenes* NCIB 9867 and *Pseudomonas putida* NCIB 9869

JOURNAL (SO): Appl. Environ. Microbiol., 65 (3), 946-950 (1999)

OTHER SOURCE (OS): CA 130:322223

REFERENCE: 51 (bases 59070 to 60560)

AUTHOR (AU): Bosch, R.; Moore, E.R.; Garcia-Valdes, E.; Pieper, D.H.

TITLE (TI): NahW, a novel, inducible salicylate hydroxylase involved in mineralization of naphthalene by *Pseudomonas stutzeri* AN10

JOURNAL (SO): J. Bacteriol., 181 (8), 2315-2322 (1999)

OTHER SOURCE (OS): CA 131:70144

REFERENCE: 52

AUTHOR (AU): DeZwaan, T.M.; Carroll, A.M.; Valent, B.; Sweigard, J.A.

TITLE (TI): Magnaporthe grisea pth11p is a novel plasma membrane protein that mediates appressorium differentiation in response to inductive substrate cues

JOURNAL (SO): Plant Cell, 11 (10), 2013-2030 (1999)

OTHER SOURCE (OS): CA 132:47358

REFERENCE: 53 (bases 122486 to 123895)

AUTHOR (AU): McCormick,S.P.; Alexander,N.J.; Trapp,S.E.; Hohn,T.M.
 TITLE (TI): Disruption of TRI101, the gene encoding trichothecene
 3-O-acetyltransferase, from *Fusarium sporotrichioides*
 JOURNAL (SO): Appl. Environ. Microbiol., 65 (12), 5252-5256 (1999)
 OTHER SOURCE (OS): CA 132:118174
 REFERENCE: 54 (bases 111907 to 113460)
 AUTHOR (AU): Muraguchi,H.; Kamada,T.
 TITLE (TI): A mutation in the *eln2* gene encoding a cytochrome P450
 of *Coprinus cinereus* affects mushroom morphogenesis
 JOURNAL (SO): Fungal Genet. Biol., 29 (1), 49-59 (2000)
 OTHER SOURCE (OS): CA 134:96073
 REFERENCE: 55 (bases 108826 to 111209)
 AUTHOR (AU): Yu,J.; Chang,P.K.; Bhatnagar,D.; Cleveland,T.E.
 TITLE (TI): Genes encoding cytochrome P450 and monooxygenase
 enzymes define one end of the aflatoxin pathway gene
 cluster in *Aspergillus parasiticus*
 JOURNAL (SO): Appl. Microbiol. Biotechnol., 53 (5), 583-590 (2000)
 OTHER SOURCE (OS): CA 133:291807
 REFERENCE: 56 (bases 122486 to 123895)
 AUTHOR (AU): Muhitch,M.J.; McCormick,S.P.; Alexander,N.J.; Hohn,T.M.
 TITLE (TI): Transgenic expression of the TRI101 or PDR5 gene
 increases resistance of tobacco to the phytotoxic
 effects of the trichothecene 4,15-diacetoxyscirpenol
 JOURNAL (SO): Plant Sci., 157 (2), 201-207 (2000)
 OTHER SOURCE (OS): CA 133:306551
 REFERENCE: 57 (bases 107279 to 108340)
 AUTHOR (AU): Cheng,Q.; Thomas,S.M.; Kostichka,K.; Valentine,J.R.;
 Nagarajan,V.
 TITLE (TI): Genetic analysis of a gene cluster for cyclohexanol
 oxidation in *Acinetobacter* sp. Strain SE19 by in vitro
 transposition
 JOURNAL (SO): J. Bacteriol., 182 (17), 4744-4751 (2000)
 OTHER SOURCE (OS): CA 134:37832
 REFERENCE: 58 (bases 100363 to 101496)
 AUTHOR (AU): Jornvall,H.; Hoog,J.O.; Persson,B.; Pares,X.
 TITLE (TI): Pharmacogenetics of the alcohol dehydrogenase system
 JOURNAL (SO): Pharmacology, 61 (3), 184-191 (2000)
 OTHER SOURCE (OS): CA 134:38655
 REFERENCE: 59
 AUTHOR (AU): Calabrese,D.; Bille,J.; Sanglard,D.
 TITLE (TI): A novel multidrug efflux transporter gene of the major
 facilitator superfamily from *Candida albicans* (FLU1)
 conferring resistance to fluconazole
 JOURNAL (SO): Microbiology (Reading, Engl.), 146 (PT 11), 2743-2754
 (2000)
 OTHER SOURCE (OS): CA 135:1055
 REFERENCE: 60
 AUTHOR (AU): Deising,H.B.; Werner,S.; Wernitz,M.
 TITLE (TI): The role of fungal appressoria in plant infection
 JOURNAL (SO): Microbes Infect., 2 (13), 1631-1641 (2000)
 REFERENCE: 61 (bases 43783 to 45994)
 AUTHOR (AU): Smith,S.
 TITLE (TI): The world according to PARP
 JOURNAL (SO): Trends Biochem. Sci., 26 (3), 174-179 (2001)
 OTHER SOURCE (OS): CA 135:15779
 REFERENCE: 62 (bases 131646 to 132375)
 AUTHOR (AU): Cronk,J.D.; Endrizzi,J.A.; Cronk,M.R.; O'Neill,J.W.;
 Zhang,K.Y.
 TITLE (TI): Crystal structure of *E. coli* beta-carbonic anhydrase,
 an enzyme with an unusual pH-dependent activity
 JOURNAL (SO): Protein Sci., 10 (5), 911-922 (2001)
 REFERENCE: 63 (bases 43783 to 45994)

AUTHOR (AU): Ziegler,M.; Oei,S.L.
 TITLE (TI): A cellular survival switch: poly(ADP-ribosyl)ation stimulates DNA repair and silences transcription
 JOURNAL (SO): Bioessays, 23 (6), 543-548 (2001)
 REFERENCE: 64 (bases 43783 to 45994)
 AUTHOR (AU): Herceg,Z.; Wang,Z.Q.
 TITLE (TI): Functions of poly(ADP-ribose) polymerase (PARP) in DNA repair, genomic integrity and cell death
 JOURNAL (SO): Mutat. Res., 477 (1-2), 97-110 (2001)
 OTHER SOURCE (OS): CA 136:145570
 REFERENCE: 65 (bases 15614 to 17392)
 AUTHOR (AU): Mundodi,S.R.; Watson,B.S.; Lopez-Meyer,M.; Paiva,N.L.
 TITLE (TI): Functional expression and subcellular localization of the Nectria haematococca Makl phytoalexin detoxification enzyme in transgenic tobacco
 JOURNAL (SO): Plant Mol. Biol., 46 (4), 421-432 (2001)
 OTHER SOURCE (OS): CA 135:285870
 REFERENCE: 66 (bases 1 to 163680)
 AUTHOR (AU): Pel,H.J.; de Winde,J.H.; Archer,D.B.; Dyer,P.S.; Hofmann,G.; Schaap,P.J.; Turner,G.; de Vries,R.P.; Albang,R.; Albermann,K.; Andersen,M.R.; Bendtsen,J.D.; Benen,J.A.; van den Berg,M.; Breestraat,S.; Caddick,M.X.; Contreras,R.; Cornell,M.; Coutinho,P.M.; Danchin,E.G.; Debets,A.J.; Dekker,P.; van Dijk,P.W.; van Dijk,A.; Dijkhuizen,L.; Driessen,A.J.; d'Enfert,C.; Geysens,S.; Goosen,C.; Groot,G.S.; de Groot,P.W.; Guillemette,T.; Henrissat,B.; Herweijer,M.; van den Hombergh,J.P.; van den Hondel,C.A.; van der Heijden,R.T.; van der Kaaij,R.M.; Klis,F.M.; Kools,H.J.; Kubicek,C.P.; van Kuyk,P.A.; Lauber,J.; Lu,X.; van der Maarel,M.J.; Meulenbergh,R.; Menke,H.; Mortimer,M.A.; Nielsen,J.; Oliver,S.G.; Olsthoorn,M.; Pal,K.; van Peij,N.N.; Ram,A.F.; Rinas,U.; Roubos,J.A.; Sagt,C.M.; Schmoll,M.; Sun,J.; Ussery,D.; Varga,J.; Verweken,W.; van de Vondervoort,P.J.; Wedler,H.; Wosten,H.A.; Zeng,A.P.; van Ooyen,A.J.; Visser,J.; Stam,H.
 TITLE (TI): Genome sequencing and analysis of the versatile cell factory *Aspergillus niger* CBS 513.88
 JOURNAL (SO): Nat. Biotechnol., 25 (2), 221-231 (2007)
 OTHER SOURCE (OS): CA 146:310276
 REFERENCE: 67 (bases 1 to 163680)
 AUTHOR (AU): Pel,H.J.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O. Box 1, 2600 MA Delft, THE NETHERLANDS

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..163680	/organism="Aspergillus niger" /mol-type="genomic DNA" /db-xref="taxon:5061" /clone="An18c0040"
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mRNA	join(<41..>325, 417..>545)	/locus-tag="An18g00920"
CDS	join(41..325,417..545)	/locus-tag="An18g00920" /codon-start=1 /product="hypothetical protein" /protein-id="CAK47170.1" /db-xref="GI:134084137"

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exon	41..325	/locus-tag="An18g00920"
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intron	326..416	/locus-tag="An18g00920"
		/number=1
exon	417..545	/locus-tag="An18g00920"
		/number=2
gene	874..954	/gene="tRNA-Arg (CCG)"
		/locus-tag="An18e00930"
tRNA	874..954	/gene="tRNA-Arg (CCG)"
		/locus-tag="An18e00930"
		/product="tRNA-Arg"
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		/note="codon recognized: CCG"
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mRNA	complement(join(<1241..1273,1325..1814,1867..2175,2229..2599,2960..>3043))	/locus-tag="An18g00940"
CDS	complement(join(1241..1273,1325..1814,1867..2175,2229..2599,2960..3043))	/locus-tag="An18g00940"
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exon	complement(1241..1273)	/locus-tag="An18g00940"
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intron	complement(1274..1324)	/locus-tag="An18g00940"


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exon      complement(1867..2175) /number=2
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intron    complement(2176..2228) /number=3
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exon      complement(2229..2599) /number=3
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intron    complement(2600..2959) /number=4
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exon      complement(2960..3043) /number=4
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gene      complement(<3788..>4775 /number=5
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)
mRNA      complement(join(<3788.. /locus-tag="An18g00950"
4122,4201..4523,
4678..>4775))
CDS        complement(join(3788..4 /locus-tag="An18g00950"
122,4201..4523,
4678..4775))

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Title: weak similarity to
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MK0549 - Methanopyrus kandle"
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                                                /protein-id="CAK47172.1"
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HTAEDRVKDKALDTEIRWAAHEKNPASHLIYVID
TETGRVAGGCEWLIHFKNPFPPNGP
QPLSCTWYPEGSEAEYASRMLSQAFFPRMCWLQ
RPHAGVNAMGVHPDYRRRGVGRLL
MQWQHERIDPLGYESWIEGSPIGRWLYEESGYKR
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exon      complement(3788..4122) /locus-tag="An18g00950"
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intron    complement(4123..4200) /locus-tag="An18g00950"
                                                /number=1
exon      complement(4201..4523) /locus-tag="An18g00950"
                                                /number=2
intron    complement(4524..4677) /locus-tag="An18g00950"
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exon      complement(4678..4775) /locus-tag="An18g00950"
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gene      complement(<5212..>7379 /locus-tag="An18g00960"
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mRNA      complement(join(<5212.. /locus-tag="An18g00960"
5456,5493..5664,
5746..6075,6140..6159,
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6800..6899,
7249..>7379))
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456,5493..5664,
5746..6075,6140..6159,
6225..6602,6674..6746,
6800..6899,7249..7379))

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sequence:PIR:S11175"
/note="unnamed protein product;
Function: Hnml of S. cerevisiae is
the unique coline permease in
yeast (Km of 0.5 micromolar).
Regulation: in S. cerevisiae,
expression of HNM1 gene is
regulated by the phospholipid
precursors inositol and choline
and this regulation involves the
trans-acting factors Ino2p, Ino4p
and Op1p. Remark: alternate name
for S. cerevisiae Hnml is YGL077c.
Similarity: Hnml of S. cerevisiae
belongs to the APC family, which
encompasses amino acid permeases
more related to the mammalian
cationic amino-acid transporter
family (Tea/ecoR). Title: strong
similarity to choline permease
Hnml -Saccharomyces cerevisiae
plasma membrane"
/citation=[12]
/citation=[19]
/citation=[24]
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SGTPSKATFSDDAYELARVGKKEV
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GGQYHWVSIAPRSARKFLSHVTG
SVCIIAWTAAPTAAIYLAASVLQSTIAMNIPSYD
PKGWHITLIMWAILLVCTVLNTWL
GMILPVIEVLILLVHVLGFFAVLVPLVYLGPKA
PRSIPTVSDYGGWGDLTLTATFIG
LKGTVAAAFVGTGDVAHMAEEVANSRVVPRSMML
ALMINGATGFALLIAFLFTAGDLL
KIVESSASYPFMYMLASSTGSKGAAVLSSMMMAI
LQACAGLAGISGSRMLWSFSREQ
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exon	complement (5746..6075)
intron	complement (6076..6139)

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exon      complement(6140..6159) /number=3
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intron    complement(6160..6224) /number=4
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intron    complement(6603..6673) /number=5
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exon      complement(6674..6746) /number=6
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intron    complement(6747..6799) /number=6
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intron    complement(6900..7248) /number=7
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exon      complement(7249..7379) /number=8
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exon      complement(8380..8415) /locus-tag="An18g00970"
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mRNA      join(<8621..8764, /locus-tag="An18g00980"
8830..9156,9214..9356,
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CDS       join(8621..8764, /locus-tag="An18g00980"
8830..9156,9214..9356,
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                                                /note="unnamed protein product;
Function: M. grisea Pth11 is a
pathogenicity gene. Function: M.
grisea Pth11p is likely to be
involved in host surface
recognition. Function: M. grisea
pth11 mutants of strain 4091-5-8
are nonpathogenic due to a defect
in appressorium differentiation.
Localization: in M. grisea, a

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		<p>Pth11-green fluorescent protein fusion localised to the cell membrane and vacuoles. Similarity: similarity of the predicted A. niger protein and M. grisea Pth11 is limited to the N-terminal half of the protein sequences. Title: weak similarity to integral membrane protein PTH11 - Magnaporthe grisea plasma membrane"</p> <p>/citation=[52] /codon-start=1 /protein-id="CAK47175.1" /db-xref="GI:134084142" /translation="MTDHSAAVKVVTCFLIVSF IAVVACLTINQVLRKRVSSVALL LSTLIASIASGAAVSVAAHGLGQASPLTDAQV VMQKALYSMEVLYVLTGLGKLSV MVLFLYLLSSTGQSKSVLAATGLLLIWMVIV VCLQCHPPEVWNIIVGGTCLDLSGI WIAFGVMNVLVEIMIIAIVPSFIIIFRLKLSLKRRL VVISCFGIRILDIAGSIVQLCYVR NFKIHADSPMPTNVWQWAICSQVLQTVAISACV PYLREFLESFSPSGMFKPTELKHT VQSAYNATKCSDDIELMRPESTKDT" /locus-tag="An18g00980" /inference="protein motif:SignalP:2.0" /locus-tag="An18g00980"</p>
sig-peptide	8621..8698	
mat-peptide	join(8699..8764, 8830..9156,9214..9356, 9406..9697)	
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intron	8765..8829	/locus-tag="An18g00980" /number=1
exon	8830..9156	/locus-tag="An18g00980" /number=2
intron	9157..9213	/locus-tag="An18g00980" /number=2
exon	9214..9356	/locus-tag="An18g00980" /number=3
intron	9357..9405	/locus-tag="An18g00980" /number=3
exon	9406..9700	/locus-tag="An18g00980" /number=4
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sig-peptide	complement(9877..9927)	

mat-peptide	complement(9790..9876)	motif:SignalP:2.0" /locus-tag="An18g00990" /product="unnamed"
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mRNA	join(<10500..10749, 10812..11041, 11105..>11479)	/locus-tag="An18g01000"
CDS	join(10500..10749, 10812..11041, 11105..11479)	/locus-tag="An18g01000" /note="unnamed protein product; Similarity: the nucleotide sequence of the ORF shows strong similarity to the ESTs an-2192 and an-2204 of <i>A. niger</i> . Title: strong similarity to EST an-2192 - <i>Aspergillus niger</i> " /codon-start=1 /protein-id="CAK47177.1" /db-xref="GI:134084144" /translation="MYSYEKVNRRDDSDQGLLAE DSERVAQPQRVSFPFSWTNALLLL GLLFLSLNLNVGVFVFKGHNVPIDLPDAAMAK QRSPTYGLAWDTHKPYSHHSEYTS ENATHADEMWESLSMDPMVIAPTWEWAQSKGLSD SWAFPWDSNRRIYFIKVFHQLHCL KLMRHSYHELWSGGQESSIPAPHIEHCLDSLRLQDL MCKADDTMPMSLQLLNGGGEGQQM QCKDFDKLVAWSKAPERNACYKRLTDYKPIVHSI ERYAFCEPDESEHYPTMSKYFEEHG HYADPFSE"
exon	10500..10749	/locus-tag="An18g01000" /number=1
intron	10750..10811	/locus-tag="An18g01000" /number=1
exon	10812..11041	/locus-tag="An18g01000" /number=2
intron	11042..11104	/locus-tag="An18g01000" /number=2
exon	11105..11479	/locus-tag="An18g01000" /number=3
gene	<11980..>13464	/locus-tag="An18g01010"
mRNA	join(<11980..12137, 12198..>13464)	/locus-tag="An18g01010"
CDS	join(11980..12137, 12198..13464)	/locus-tag="An18g01010" /inference="profile:COGS:COG0477" /note="unnamed protein product; Function: FLU1 of <i>C. albicans</i> facilitates resistance to fluconazole and cycloheximide in the fluconazole-hypersensitive <i>S.</i> <i>cerevisiae</i> strain YKKB-13 lacking the ABC (ATP-binding cassette) transporter gene PDR5. Function: FLU1 of <i>C. albicans</i> facilitates resistance to mycophenolic acid in <i>C. albicans</i> . Function: FLU1 of <i>C.</i> <i>albicans</i> is involved in the resistance to azol derivatives in <i>C. albicans</i> . Function: MDR1 of <i>C.</i>

		albicans facilitates resistance to the anti-mitotic drug benomyl and to the dihydrofolate reductase inhibitor methotrexate. Similarity: N-terminus of the A. niger protein is app. 120 aa shorter than in FLU1 of C. albicans. Similarity: the predicted A. niger protein shows strong similarity to fluconazole resistance protein FLU1 of C. albicans, which is a permease belonging to the major facilitator superfamily. Title: strong similarity to fluconazole resistance protein FLU1 - Candida albicans" /citation=[59] /codon-start=1 /protein-id="CAK47178.1" /db-xref="GI:134084145" /translation="MDEEDGHCKETEVTVQSTSP VDSADYDPFDPQTRSTTYKWITVV LVAGLSTMVQLSTIIAAPVSPSILAHFHSNALLY RTLIVSIWELGEIVAPLLWGLSE LYGRQWPLNIANLFFVAFLAGTAASTSIQMLIAF RFLSGAATAASAIGFPGIVSDLFPE ESRGRAMSIMSLTGALGPVVGPIIGSYLGEKAGW RWAFLWPTIATGTLSELLIVVYRE TYSVTLQKRKARQQNPESGSKSPEDTDKTASQVF FKAILRPLRLLIRSPMLILVTFYL SVVYGYTYLVMTTIAPLFQDVYGFSEGLAFL GLCLGLILGAFLLCSFLLDYRVRTA RARSGTSKPEQRLPPVLIACFVMSGGLFLFGWTA QYHVQWIAPIIGTGIIGFGLVSTT ITLQTYVVDLFGIYAASATSAMLVPRNACAAFLP LAGPPLFDRLGYNWGGTLLALIVL VFSLMPLIFINYGRLRGKNLLDD" /locus-tag="An18g01010" /number=1 /locus-tag="An18g01010" /number=1 /locus-tag="An18g01010" /number=2 /locus-tag="An18g01020" complement(<14029..>151 72) complement(join(<14029.. .14318,14411..14845, 14917..>15172)) complement(join(14029.. 14318,14411..14845, 14917..15172)) /EC-number="1.13.11.4" /inference="profile:COGS:COG3435" /inference="similar to AA sequence:UniProtKB:AF173167.3" /note="unnamed protein product; Complex: the estimated molecular mass of the purified gentisate 1, 2-dioxygenase of P. alcaligenes was 154 kDa, with a subunit mass of 39 kDa. its structure is
exon	11980..12137	
intron	12138..12197	
exon	12198..13464	
gene	complement(<14029..>15172)	
mRNA	complement(join(<14029.. .14318,14411..14845, 14917..>15172))	
CDS	complement(join(14029.. 14318,14411..14845, 14917..15172))	

deduced to be a tetramer. Remark:
 gentisate 1,2-dioxygenase of *P. alcaligenes* exhibits typical
 saturation kinetics and has an
 apparent K_m of 92 μM for
 gentisate. this enzyme has broad
 substrate specificities towards
 alkyl and halogenated gentisate
 analogs. Similarity: the predicted
A. niger protein shows strong
 similarity to gentisate
 1,2-dioxygenase of *P. alcaligenes*
 and conserved hypothetical
 proteins from other procaryotic
 species. Title: strong similarity
 to gentisate 1,2-dioxygenases xlnE
 - *Pseudomonas alcaligenes*"

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 MQKGDVILPTWNYHDHKGDTGTF
 MIWLDGLDLNFRHFPVHFVDHYDQPRYPADVD
 SATSPIVFPWDMKAELDKAPGTW
 AVRRYLADSGEGSQAERVDAGTSSLPRQETTSA
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gene	<15614..>17392	/locus-tag="An18g01030"
mRNA	join(<15614..15661, 15723..16281, 16347..16503, 16584..16739, 16803..16942, 17034..>17392)	/locus-tag="An18g01030"
CDS	join(15614..15661, 15723..16281, 16347..16503, 16584..16739, 16803..16942, 17034..17392)	/locus-tag="An18g01030"

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/inference="profile:PFAM:PF01360"
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 Function: Mak1 from N.
 haematococca specifically
 hydroxylates the phytoalexins
 medicarpin and
 maackiain, converting them to less
 fungitoxic derivatives.
 Localization: heterologous
 expression of the Mak1 cDNA
 construct in plants indicated that
 Mak1 protein accumulates in the
 plant cytoplasm, associated with
 endoplasmic reticulum membranes.
 Similarity: the predicted A. niger
 protein shows strong similarity to
 Mak1 from the fungal pathogen N.
 haematococca. Mak1 belongs to the
 flavin-containing mono-oxygenases.
 best matches are with putative
 salicylate hydroxylases of several
 procaryotic species. Title: strong
 similarity to maackiain
 detoxification protein 1 MAK1 -
 Nectria haematococca endoplasmatic
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exon	16584..16739

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intron	16943..17033	/number=5
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exon	17034..17392	/number=5
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mRNA	join(<17766..17864, 17939..18039, 18108..18343, 18398..19163, 19373..19935, 20037..20252, 20325..>20491)	/locus-tag="An18g01040"
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CDS	join(17766..17864, 17939..18039, 18108..18343, 18398..19163, 19373..19935, 20037..20252, 20325..20491)	/locus-tag="An18g01040"

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 sequence:UniProtKB:ENU56097.1"
 /note="unnamed protein product;
 Phenotype: facB recessive loss of
 function mutants in A. nidulans
 are deficient in acetate induction
 of acetyl-CoA synthase, isocitrate
 lyase, malate
 synthase, acetamidase, and
 NADP-isocitrate dehydrogenase.
 Similarity: the predicted A. niger
 protein shows similarity to
 acetate regulatory DNA binding
 protein FacB (facB) from A.
 nidulans, which belongs to the
 GAL4-type zinc cluster
 transcriptional activators. Title:
 similarity to acetate regulatory
 DNA binding protein facB -
 Aspergillus nidulans"
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 DAPRKENPLSNQSERFSDFAGTETIDAMGAVAF
 ADEEDCGFFGPSNIAFLRLHLSCA
 VAHSASAQKEIITSPPLDRVAYDGGFVSATRPSSP
 SHDQRPESLEGEKFDKALPPPEE
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 SGTTSAETGISESAIYYHRALSCKGEILRGTTL
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 QLGLHSGKASRAFTPLEQEVKRRT

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 IERSEVGDEGHHKLYPLKFRIILT
 LRYFHVQILLHRPILVKFLDATGPSGLEADEVKL
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 Catalytic activity:
 lignostilbene-alpha,beta-dioxygenase
 isozymes (LSD-I, II, and III)
 of *P. paucimobilis* catalyse the
 reaction
 1,2-bis(4-hydroxy-3-methoxyphenyl)
 ethylene + O(2) = 2 vanillin

Cofactor:
lignostilbene-alpha,beta-dioxygenase isozymes (LSD-I, II, and III) of *P. paucimobilis* require iron as a cofactor. Complex: LSD-I, II, and III consist of alpha, alpha, alpha, and beta subunits, respectively. they show different specificities for several substrates that are stilbene and styrene derivatives. Function: LSD of *P. paucimobilis* catalyses the oxidative cleavage of the interphenyl double bond in the synthetic substrate and lignin-derived stilbenes. it is responsible for the degradation of a diarylpropane-type structure in lignin. Similarity: the predicted *A. niger* protein shows strong similarity to subunit lsdB of lignostilbene-alpha,beta-dioxygenase isozyme LSD-III of *P. paucimobilis* and related dioxygenases from several plant species. Title: strong similarity to subunit lsdB of lignostilbene-alpha,beta-dioxygenase isozyme LSD-III -*Pseudomonas paucimobilis*"
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IVYFNGQLLALKEDSPPYAMDPVT
LETGRGLYDFDGLPMTFTAHKPKFDPETGEMICEF
GYEARGDGTDPVCYYTVGPDGKFT
EVVWLVAPVVMVMIHDFAVTDNWWVIFPIIPQLCDI
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RRGAKTADVWKFQYKNSFFPGHTANAHEDSSGNLI
IDLGLSEKNVFFWPDQAQGNAPEP
SSIRSQLVRFTINPRAEDLNLTEPRILQADNSEF
YRIDRYATKPHRHVFFMDMPDPSL
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exon complement(21501..21638
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Catalytic activity:
5-carboxymethyl-2-hydroxymuconate
delta-isomerase from E. coli
catalyses the reaction
5-carboxymethyl-2-hydroxymuconate
= 5-carboxy-2-oxohept-3-enedioate.
Pathway:
5-carboxymethyl-2-hydroxymuconate
delta-isomerase from E. coli is
involved in tyrosine and
phenylalanine metabolism.
Similarity: the predicted A. niger
protein shows strong similarity to
5-carboxymethyl-2-hydroxymuconate
delta-isomerase from E. coli and
many putative
2-hydroxyhepta-2,4-diene-1,
7-dioate isomerases from several
prokaryotic and eucaryotic
organisms. Title: strong
similarity to
5-carboxymethyl-2-hydroxymuconate
delta-isomerase -Escherichia coli
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CDS	join(24984..25058, 25166..25301, 25564..25745, 25812..26003, 26080..26144, 26206..26646, 26722..27303, 27423..27426)	

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/note="unnamed protein product;
Function: FLU1 of C. albicans
facilitates resistance to
fluconazole and cycloheximide in
the fluconazole-hypersensitive S.
cerevisiae strain YKKB-13 lacking
the ABC (ATP-binding cassette)
transporter gene PDR5. Function:
FLU1 of C. albicans facilitates
resistance to mycophenolic acid in
C. albicans. Function: FLU1 of C.
albicans is involved in the
resistance to azol derivatives in
C. albicans. Function: MDR1 of C.
albicans facilitates resistance to
the anti-mitotic drug benomyl and
to the dihydrofolate reductase
inhibitor methotrexate.
Similarity: N-terminus of the A.
niger protein is app. 120 aa
shorter than in FLU1 of C.
albicans. Similarity: the
predicted A. niger protein shows
strong similarity to fluconazole
resistance protein FLU1 of C.
albicans, which is a permease
belonging to the major facilitator
superfamily. Title: similarity to
fluconazole resistance protein

FLU1 - *Candida albicans*"
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 intron 25746..25811
 exon 25812..26003
 intron 26004..26079
 exon 26080..26144
 intron 26145..26205
 exon 26206..26646
 intron 26647..26721
 exon 26722..27303
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 28602..>28667))
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protein shows strong similarity to the protein sequences lysophospholipase (sequence 5 and sequence 7) of patents WO0127251-A/5 and WO0127251-A/7 from A. oryzae (AC# AX112082 and AC# AX112084) and to other fungal lysophospholipases. Title: strong similarity to lysophospholipase from patent WO0127251-A - Aspergillus oryzae extracellular/secretion proteins" /citation=[14] /codon-start=1 /protein-id="CAK47186.1" /db-xref="GI:134084153" /translation="MLSLLISAAAATLASALELP QGYSPDPVSCPTNLSWIRPAVGLS RDEAQWVEGRKNVILGSLDAYLKRNLNDDFDTE YISRLNNTSQTPIMGMAISGGGFG SAYTGTGLIRALDDRLPAANEQRTGGLLQSMYTL SGLSGGSWPAVSFFSYNFTADEI VDYWKPEIDRFFTVINTSAEAAATGKAIFEQIATK YLAGFEVALSDYLGRGFAYEFIPG QSGGLNTTFSGIRNLSNFINHQMPFIIHLASVE PEDAEYYDLLVPSSNGIIFDLTPF EFGAWGDVHAFPTFEWLGNLQNSGIPVQSKCW KGFDRSSLVIGTSADAFNFWYLES VSNGLTGQFAKRSTTHESSLTKRSLQPANLNALV DAFQETFDLNLTIQISYKFPNPFT NLSLSTGNTHKSSSTLNLVDGSETGQTIPLWGQIQ PARNVDFIIAWDDSQDADPYSWNN GTNLYNTYLAANATGLPFPIIPPSRTMMNLNYTL HPQFFGCDANLTTTGDDRAPIVLY MANAPYSAYTNFSFWQTETSRQQMGEIFVNSFDI VTQANGSWDGEWAECMGAVERS LARVGMERTRQCRCFCERYCWDGTLDERDPGVLD PTLVLDPGVKFGLWATNPY" /locus-tag="An18g01090" /inference="protein motif:SignalP:2.0" /locus-tag="An18g01090" /product="unnamed" /locus-tag="An18g01090" /number=1 /locus-tag="An18g01090" /number=1 /locus-tag="An18g01090" /number=2 /locus-tag="An18g01090" /number=2 /locus-tag="An18g01090" /number=3 /locus-tag="An18g01100" 18) complement(join(<30960..>322 /locus-tag="An18g01100" .31045,31081..31220, 31273..31630, 31702..>32218)) complement(join(30960.. /locus-tag="An18g01100"

sig-peptide 28874..28921

mat-peptide join(28922..29683, 29736..29875, 29925..30834)

exon 28874..29683

intron 29684..29735

exon 29736..29875

intron 29876..29924

exon 29925..30837

gene complement(<30960..>322 18)

mRNA complement(join(<30960..>32218))

CDS complement(join(30960..>32218))

31045,31081..31220,
31273..31630,
31702..32218)

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/inference="profile:PFAM:PF00107"
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Remark: the patent does not
provide further information about
the function of the protein.
Similarity: the predicted A. niger
protein shows strong similarity to
the protein sequence alcohol
dehydrogenase (sequence 19) of
patent EP0845532-A/19 from an
unclassified organism (AC# A92108)
and to other zinc-containing
dehydrogenases. Title: strong
similarity to alcohol
dehydrogenase from patent
EP0845532-A - Unclassified
organism cytoplasm"
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KGMRIQTVLVQGTGGVSMFALKLALAAGLRVVL
TSSDAKLQAIKEKYAGSAILTVN
YKNTEPWEDEVLKLTGGVVDLVVENGGTGSLVK
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77)
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35095..35477))

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                               Catalytic activity: versicolorin B
                               synthase from A. parasiticus
                               catalyses the side chain
                               cyclization of racemic versiconal
                               hemiacetal to the bisfuran ring
                               system of(-)-versicolorin B.
                               Pathway: versicolorin B synthase
                               from A. parasiticus is involved in
                               the aflatoxin biosynthetic
                               pathway. Remark: a splice site was
                               detected upstream of the START
                               codon. Remark: aflatoxins comprise
                               a group of polyketide-derived
                               carcinogenic mycotoxins. Remark:
                               the genes encoding the aflatoxin
                               biosynthetic enzymes in A.
                               parasiticus are clustered. Remark:
                               versicolorin B synthase from A.
                               parasiticus possesses an
                               amino-terminal sequence homologous
                               to the ADP-binding region of other
                               flavoenzymes, but does not require
                               flavin or nicotinamide cofactors
                               for its cyclase activity.
                               Similarity: the predicted A. niger
                               protein shows strong similarity to
                               versicolorin B synthase from A.
                               parasiticus and other
                               oxidoreductases. Title: strong
                               similarity to versicolorin B
                               synthase vbs - Aspergillus
                               parasiticus"
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TLFFYKNQKFTTPNTQIRAKNATGYDSPAYES
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SSEESFLANKSTLITYTIANLAKK
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GAFQSPQLLMVSGVGGPDQLEEHG
IQOVNFAIRPGVGNLMDHPFFAFPSYRVNVQFTTAI
ANDFLFIVGQFINMVGFGNGPLTN
PISDYLAWEKIPAAALRASAFSSQTKQLATFPSSD
PEAEYSISGAGMYGNVSNLLINOPE
DGQYASMLAVLITPTSRNITLRSADTDLDPV
NPNWLTALQSDQEVAIAMFKRRVRA
FQSKAMAPVITIGNEYNFGVLGSEDEQLQWIKIND
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		Remark: the patent does not
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		the function of the protein.
		Similarity: the predicted A. niger
		protein shows similarity to the
		protein fragment (SEQ ID NO:
		51484) of patent EP1033405-A2 from
		A. thaliana (AC# AAG41385) and to
		putative sterol desaturase family
		proteins. Title: similarity to
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		from patent EP1033405-A2 -
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		LIAIHQLQVMRRMGHVLGFLDGDQHRDGVDPVG
		VAKVVRSLISTSFPRIMTVFLSY
		RVSQAPAQMSWGWLFEIGLYGIILDFWFWYHHR
		LMHDVGSGLWKYHRTTHLTKHPNPL
		LTLYADTEQEFFDIAGIPLMTYFSMRMLGMPMGF
		YEWWICHQYVVFTELAGHSGLRMH
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		/inference="profile:PFAM:PF02558"
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		/citation=[23]
		/citation=[42]
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		RHSVICLFQNLGQIEELNERLFTDPLTRPTYMF
		GIMRHGVYIKAPFEAVLAGLTGSC
		ALGIVNNDQQASSLSASSTASQSRFLINRLVEA
		PIVRSSSELPWMLHQAQLKLATN
		CVVNPLTALLDVRNGSLLANSELQEMRRQLQEI
		SLVFRRLPEFQGLPDVEEQFSVAR
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mRNA	join(<40728..41152, 41226..42344, 42401..>42671)	/locus-tag="An18g01150"
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/inference="profile:COGS:COG0477"
 /inference="similar to AA
 sequence:UniProtKB:AF188621.1"
 /note="unnamed protein product;
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 facilitates resistance to
 fluconazole and cycloheximide in
 the fluconazole-hypersensitive S.
 cerevisiae strain YKKB-13 lacking
 the ABC (ATP-binding cassette)
 transporter gene PDR5. Function:
 FLU1 of C. albicans facilitates
 resistance to mycophenolic acid in
 C. albicans. Function: FLU1 of C.
 albicans is involved in the
 resistance to azol derivatives in
 C. albicans. Function: MDR1 of C.
 albicans facilitates resistance to
 the anti-mitotic drug benomyl and
 to the dihydrofolate reductase
 inhibitor methotrexate.
 Similarity: the predicted A. niger
 protein shows strong similarity to
 fluconazole resistance protein
 FLU1 of C. albicans, which is a
 permease belonging to the major
 facilitator superfamily. Title:
 strong similarity to fluconazole
 resistance protein FLU1 - Candida
 albicans"
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 AIFSSSTTNVARVFGVGIEVATLSSSLYICGYAS
 GPLVWAPLSLKGKRPPIVVMVLG
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		/note="codon recognized: CAC"
gene	<43783..>45994	/locus-tag="An18g01170"
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CDS	join(43783..43852, 43912..44025, 44075..44344, 44395..45240, 45294..45376, 45425..45994)	/locus-tag="An18g01170" /EC-number="2.4.2.30" /inference="profile:PFAM:PF00644" /inference="profile:PFAM:PF02877" /note="unnamed protein product; Catalytic activity: the NAP protein of Z. mays catalyses the reaction NAD(+) + {ADP-D-ribosyl} (N)-acceptor <=> nicotinamide + {ADP-D-ribosyl} (N+1)-acceptor. Function: the NAP protein of Z. mays is involved in programmed cell death or apoptosis. Localization: the NAP protein of Z. mays is a nuclear enzyme. Remark: the ADP-D-ribosyl group of NAD(+) is transferred to an acceptor carboxyl group on a histone or the enzyme itself, and further ADP-ribosyl groups are transferred to the 2'-position of the terminal adenosine moiety, building up a polymer with an

average chain length of 20-30 units. Remark: the NAP polynucleotide sequences can be used for modulation of programmed cell death in eukaryotic cells. the method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc., or during transformation). particular applications are generation of plants that are resistant to fungi or nematodes; are male or female sterile; or have better seed-shatter properties. the methods are also used to improve growth of transformed plant cells (and derived calli or complete plants). Similarity: the predicted A. niger protein shows strong similarity to the protein sequence poly(ADP-ribose) polymerase NAP protein of patent WO200004173-A1 from Z. mays (AC# AAY68834) and from many other eucaryotic organisms. Title: strong similarity to poly(ADP-ribose) polymerase NAP protein from patent WO200004173-A1 - Zea mays nucleus"

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DDEPESPKKRTLEQALGINEDGTTKKLKDAQTVG
TKQINVPVDDTCPLRLTFTVYIDP
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TWTWGRVGEHQHALLGGGGLDE
AEYEFKKFKDKSGLTWNRLDPPKKGKYTFIEK
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exon 43783..43852
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 exon 45294..45376
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 mRNA join(<46879..48454,
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 oxysporum is used for the
 enzymatic hydrolysis of penicillin
 V (phenoxy-methylpenicillin) to
 6-aminopenicillanic acid (6-APA).
 6-APA is the active beta-lactam
 nucleus used in the manufacture of
 semi-synthetic penicillins.
 Similarity: the predicted A. niger
 protein shows strong similarity to
 the protein sequence penicillin V
 amidohydrolase (PVA) of patent
 US5516679-A from F. oxysporum (AC#
 AAW00291). Title: strong
 similarity to penicillin V
 amidohydrolase PVA from patent
 US5516679-A - Fusarium oxysporum
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 GGLAAGIIGLAPAHFVQGYATAATDGGTLTLNGT

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SWTNAFWEGIDKTDGADVDEFYRV		
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tRNA	complement(48889..48960)	/gene="tRNA-Ala (AGC)"
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		/inference="similar to AA
		sequence:UniProtKB:AFU81806.1"
		/note="unnamed protein product;
		Function: orl of A. flavus
		converts O-methylsterigmatocystin
		to aflatoxin B1. Pathway: orl of
		A. flavus catalyzes the last step
		of the aflatoxin biosynthetic
		pathway. Remark: aflatoxins
		comprise a group of
		polyketide-derived carcinogenic
		mycotoxins. Similarity: the
		predicted A. niger protein shows

strong similarity to
O-methylsterigmatocystin
(OMST)-oxidoreductase (ord1) from
A. flavus, which belongs to the
CYP64 family of cytochrome
P450-type monooxygenases. Title:
strong similarity to
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oxidoreductase ord1 - Aspergillus
flavus"
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FRATRKNLHREIGSNVSVARFNEI
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exon	49850..49888
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exon	50233..50362
intron	50363..50418
exon	50419..50614
intron	50615..50701
exon	50702..50828
intron	50829..50882
exon	50883..51127
intron	51128..51198
exon	51199..51470
intron	51471..51537
exon	51538..51919

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20) /locus-tag="An18g01210"
mRNA      complement(join(<52148.. /locus-tag="An18g01210"
.52359,52411..52573,
52635..52939,
52984..53309,
53368..>53720))
CDS       complement(join(52148.. /locus-tag="An18g01210"
52359,52411..52573,
52635..52939,
52984..53309,
53368..53720))

/inference="profile:COGS:COG0515"
/inference="profile:PFAM:PF00069"
/note="unnamed protein product;
Function: SRPK2 from M. musculus
phosphorylates SF2/ASF, a member
of SR splicing factors. Remark:
overexpression of murine SRPK2
causes disassembly of
cotransfected SF2/ASF and
endogenous SC35. SRPK family
members may regulate the
disassembly of the SR proteins in
a tissue-specific manner.
Similarity: the predicted A. niger
protein shows similarity to SRPK2
from M. musculus and strong
similarity to putative
serine/threonine protein kinases
from several eucaryotic organisms.
Title: similarity to
SR-protein-specific kinase SRPK2 -
Mus musculus nucleus"
/citation={39}
/codon-start=1
/protein-id="CAK47196.1"
/db-xref="GI:134084163"
/translation="MAGRITQCARRLGLLHAKLH
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IRYSSQWKSSTLVFPTTDALIDPSIEIEETLPT
YHPEKYYPVQQGEVLNRYQVLAK
LGYGVTSTVWLGRDLRDSKYVVLKIYVTGQEKNH
ELEIYNRMNAVEVEHPGRDLVRRLL
FDHFTVTGPHGPHVCLVHEPMGMSADTLQLKYIP
GNTMTLDMEKTCIRQLLIALLDLFLH
SAARIVHTGKDLQLKNLLPVPNTKTLETLEERE
VNDSPSPRKILKDRITLYLSTVYNPG
GSGPLISDFGEARFGDVEKRDDIMPNNMYRAPEV
VLKENWNYKVDIWNVAMVANDIVI
PRHMFDRGNADGIFDDRHVHIAEMIALMGPPPASF
RERCRLAYVFVWDEQGNWKKDLAPIP
DISLESLGADIPGENREGFFRWLRKALQWNAEDR
PTATEFLFDWEWLMEGLRRPNNEDA KT"

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intron    complement(52360..52410 /locus-tag="An18g01210"
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exon      complement(52411..52573 /locus-tag="An18g01210"
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exon        complement(52635..52939 /number=2
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intron      complement(52940..52983 /number=3
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intron      complement(53310..53367 /number=4
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exon        complement(53368..53720 /number=4
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gene        complement(<54105..>557 /number=5
62)         /locus-tag="An18g01220"
mRNA        complement(join(<54105. /locus-tag="An18g01220"
.54731,54787..55334,
55392..55500,
55559..>55762))
CDS         complement(join(54105.. /locus-tag="An18g01220"
54731,54787..55334,
55392..55500,
55559..55762))

/inference="profile:COGS:COG0477"
/inference="similar to AA
sequence:PIR:S64826"
/note="unnamed protein product;
Function: in S. cerevisiae,
mutants (dal5) that lack
allantoate transport have been
isolated. these strains also
exhibit a 60% loss of allantoin
transport capability. Regulation:
in S. cerevisiae Dal5 appears to
be sensitive to nitrogen
catabolite repression, feedback
inhibition, and trans-inhibition.
Regulation: in S. cerevisiae
allantoate uptake is constitutive.
Similarity: the predicted A. niger
protein shows strong similarity to
allantoate permease gene (DAL5)
from S. cerevisiae, which belongs
to the major facilitator
superfamily. Title: strong
similarity to allantoate permease
Dal5 - Saccharomyces cerevisiae"
/citation=[7]
/citation=[9]
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/db-xref="GI:134084164"
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AVEYLQGHAAADSPQIDLRALRRK
IDWHLIPFMFSCYVLQFLDKVMLNYYAAVMGMKTE

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 GFQHVHHGATLAGWRIMFLVIGLV
 TVLIGVLTLFLIPDTPMKAKWLSSEEEKVALLQHV
 SVNQGTGVWSSAINLKQIWEGVLDI
 QLWLLVLITILISVSSGVVTYTSATLIAGFGYSG
 FISALLNMPSGIVSIFFTLLVGFG
 IRRTSRHWANAFCTIPGIIGGGLLSFLPKSNKA
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 ANCAGHTKRAFSSALIAGSFSVGNIIIGPQTFQAR
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intron    complement(55501..55558 /locus-tag="An18g01220"
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mRNA      join(<56384..56645, /locus-tag="An18g01230"
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57430..57711,
57897..58158,
58326..>58444)
CDS       join(56384..56645, /locus-tag="An18g01230"
56694..56761,
56818..57009,
57069..57368,
57430..57711,
57897..58158,
58326..58444)

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/note="unnamed protein product;
 Function: M. grisea Pthll is a
 pathogenicity gene. Function: M.
 grisea Pthllp likely is involved
 in host surface recognition.
 Function: M. grisea pthll mutants
 of strain 4091-5-8 are
 nonpathogenic due to a defect in
 appressorium differentiation.
 Localization: in M. grisea, a
 Pthll-green fluorescent protein

fusion localised to the cell membrane and vacuoles. Similarity: similarity of the predicted A. niger protein and M. grisea Pth11 is limited to the N-terminal half of the protein sequences. Title: similarity to integral membrane protein PTH11 - Magnaporthe grisea plasma membrane"

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IIYSALCVAQSRYGSLPLSLRPFK
ADLPDYTKLNYAGRFFYQLGIAGFKASLCLNYLR
LISGTSKNFYRILIWAVIAVSTLG
HLAGTLVLIFDCQPVERAWNPINISGSLPAGPTF
YGLAIFTIICDITIIILPIPLLLQ
LNIKTAQKAGVVCLFLLGLFTTICISILRLTQIHR
VAYDGNSTMLVLWGTIEFNVGNI
VTCVPFLAPLLKGAVRDFRSYSGRKGYDSRSYAL
QTWSKDFRSQRLRSTTSAAPQPKRT
PSEELILESGGVDEGGIHMIVELRVSLKRPTE
HDGINSAYASQDQIRPGSYWVDVT
DTSQWSRAEQARPTVPDGIFPAIKPSSIQEESCA
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intron	58159..58325	/locus-tag="An18g01230"
		/number=6
exon	58326..58444	/locus-tag="An18g01230"
		/number=7
gene	<59070..>60560	/locus-tag="An18g01240"
mRNA	join(<59070..59441, 59521..59806, 59879..60178, 60237..60312,	/locus-tag="An18g01240"

CDS	60374..>60560) join(59070..59441, 59521..59806, 59879..60178, 60237..60312, 60374..60560)	/locus-tag="An18g01240" /inference="profile:COGS:COG0654" /inference="profile:PFAM:PF01360" /note="unnamed protein product; Catalytic activity: NahW of P. stutzeri catalyzes the conversion salicylate + NADH + O(2) <=> catechol + NAD(+) + H(2)O + CO(2). Pathway: NahW of P. stutzeri is involved in the metabolism of naphtalene and salicylates (lower naphtalene degradation pathway). Similarity: the predicted A. niger protein shows similarity to salicylate hydroxylase (nahW) of P. stutzeri, which belongs to the NADH-dependent monooxygenase superfamily. Title: similarity to salicylate hydroxylase nahW -Pseudomonas stutzeri" /citation=[51] /codon-start=1 /protein-id="CAK47199.1" /db-xref="GI:134084166" /translation="MDDLPLVIVGAGISGLLLAQ HLQKLGVPIKIFERDAIDARSGG WGLTLHWALPALRELLPDHLVQRLPEAYVNKAA ARGDTGRFSFFDLKTGSALYSVEA AERIRVSRVRLRQLVATGLDVQWNKTLQNIESTA DTVTAHFADGTSYTGCLLIGCDGS RSPTREILYPDSHEMNPLFPVQLGAATLYTADEM AGAAEIDPFIQGSHPESNVLF SILDTPNNFVESKDKYECQIILSWADSKDIAVP SDNGERIALMKSLASDWAEFFRTL VHRLSEDTARSIRIADWMFRPLQNRSHPRVVL GDSAHMTMTYRGEGANNAIVDVL LTQRVDMRSLGTMSTQALRDALDAYENDVFRAE PSVLNSRQACVDAHDFTRILDESP LVSARVLKEDTTEQ" /locus-tag="An18g01240" /inference="protein motif:SignalP:2.0" /locus-tag="An18g01240"
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exon	59879..60178	/locus-tag="An18g01240"

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CDS	complement(join(60793..61039,61120..61169))	/locus-tag="An18g01250"
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intron	complement(61040..61119)	/locus-tag="An18g01250"
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exon	complement(61120..61169)	/locus-tag="An18g01250"
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gene	complement(61713..61825)	/gene="tRNA-Leu (CAG) "
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tRNA	complement(61713..61825)	/gene="tRNA-Leu (CAG) "
		/locus-tag="An18e01260"
		/product="tRNA-Leu"
		/inference="profile:tRNAscan:1.4"
		/note="codon recognized: CUG"
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CDS	join(61921..61955,62098..62425)	/locus-tag="An18g01270"
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exon	61921..61955	/locus-tag="An18g01270"
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intron	61956..62097	/locus-tag="An18g01270"
		/number=1


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CDS       complement(join(64435.. /locus-tag="An18g01280"
64754,64947..65072,
65109..65228,
65472..65520))

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EGPRGAANASRKPASESESGSGFH
PRPWKQNASRAGRVSPLSLVPNFFASCLYLIV
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FFIATTIRCGVPLREKGMIRVITSYRATVTRRED
KEASNLKSHGLLWGCLFQKEDQSK
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PYAVESWKAR"

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exon      complement(65109..65228 /locus-tag="An18g01280"
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intron    complement(65229..65471 /locus-tag="An18g01280"
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                                   /number=3
exon      complement(65472..65520 /locus-tag="An18g01280"
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                                   /number=4
gene      <66055..>67388        /locus-tag="An18g01290"
mRNA      join(<66055..66654,    /locus-tag="An18g01290"
66723..>67388)
CDS       join(66055..66654,    /locus-tag="An18g01290"
66723..67388)

                                   /note="unnamed protein product;
                                   Title: strong similarity to
                                   hypothetical protein encoded by
                                   An13g01340 - Aspergillus niger"
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                                   /translation="MLSLAIQSLLEADAHAASP
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exon	66723..67388	
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mRNA	<68231..>69040	
CDS	68231..69040	
exon	68231..69040	
gene	69096..69207	
tRNA	69096..69207	

gene	<71863..>73356	/locus-tag="An18g01320"
mRNA	join(<71863..72033, 72097..72406, 72467..>73356)	/locus-tag="An18g01320"
CDS	join(71863..72033, 72097..72406, 72467..73356)	/locus-tag="An18g01320"

/EC-number="3.4.23.35"
 /inference="profile:PFAM:PF00026"
 /note="unnamed protein product;
 Function: BAR1 of *S. cerevisiae*
 selectively cleaves the
 6-Leu-|-Lys-7 bond in the
 pheromone alpha-mating factor.
 BAR1 activity is abolished by in
 vitro mutation of an aspartic acid
 predicted to be in the active
 site. Induction: secretion of BAR1
 of *S. cerevisiae* is stimulated to
 as much as five times the basal
 level by exposure of cells to
 alpha-factor. Localization: BAR1
 of *S. cerevisiae* is secreted into
 the periplasmic space of MATa
 cells. Remark: BAR1 of *S.*
cerevisiae is already active in
 early compartments of the
 secretory pathway. Bar1 protease
 tolerates large N-terminal
 extensions of its substrate and
 does not require Golgi-specific
 modifications such as outer-chain
 glycosylation for activity.
 Remark: the protein sequence of
 barrier protease BAR1 of *S.*
cerevisiae is covered by patent
 WO9118988-A (AC# AAR20109). the
 patented barrier protease is
 useful in industrial processes
 where leucine-lysine or
 leucine-arginine cleavage is
 required at low pH or high
 temperature. barrier protease may
 also be used in the production and
 isolation of proteins made by
 genetic engineering methods, e. g.
 to cleave fusion proteins at
 Leu-Arg bonds. Similarity: the
 predicted *A. niger* protein shows
 strong similarity to extracellular
 protease precursor BAR1 of *S.*
cerevisiae which belongs to the
 subfamily A1 of aspartic-type
 peptidases. Title: strong
 similarity to extracellular
 protease precursor Bar1 -
Saccharomyces cerevisiae
 extracellular/secretion proteins"
 /citation=[2]
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intron	72407..72466	<pre> /locus-tag="An18g01320" /number=2 </pre>
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		except for a claim of phytase
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		strong similarity to protein
		sequence 11 from patent
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 Remark: HA protein regulates
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 glutamicum HA genes (I) can be
 used in vectors for expression in
 host cells and production of fine
 chemicals, such as, an organic
 acid, proteinogenic or
 nonproteinogenic amino acid
 (preferred), purine or pyrimidine
 base, nucleoside, nucleotide,
 lipid, saturated or unsaturated
 fatty acid, diol, carbohydrate,
 aromatic compound, vitamin,
 cofactor, polyketide or enzyme.
 the amino acids produced can be
 lysine, glutamine,
 glutamate,alanine, aspartate,
 glycine, serine, threonine,
 methionine,cysteine, valine,
 leucine, isoleucine, arginine,
 proline,histidine, tyrosine,
 phenylalanine, or tryptophan. the
 fine chemical production can be
 modulated. the presence of (I) or
 HA proteins encoded by then are
 used for diagnosing the presence
 or activity of Corynebacterium

diphtheriae. (I) can be used to map the C. glutamicum genome or can be used as markers for genetically engineered Corynebacterium or Brevibacterium. the HA proteins encoded by the (I) are used to maintain homeostasis in C. glutamicum or help the microorganism to adapt to different environmental conditions. Similarity: the predicted A. niger protein shows strong similarity to HA protein sequence SEQ ID NO:420 from patent WO200100842-A2 (AC# AAB79232), which is a monooxygenase by similarity. Title: strong similarity to HA protein sequence SEQ ID NO:420 from patent WO200100842-A2 - Corynebacterium glutamicum"
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manner similar to that of other genes in the allantoin pathway. Repression: DUR3 expression is highly sensitive to nitrogen catabolite repression and also has a partial requirement for the GLN3 product. Repression: maintenance of *S. cerevisiae* DUR3 mRNA at uninduced, nonrepressed basal levels requires the negatively acting DAL80 gene product. Similarity: *S. cerevisiae* DUR3 belongs to the major facilitator family. Title: strong similarity to urea transport protein Dur3 - *Saccharomyces cerevisiae* plasma membrane"

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Function: YCF1 from S. cerevisiae
is required for cadmium
resistance. S. cerevisiae cells
harboring a deletion of the YCF1
gene are hypersensitive to cadmium
compared with wild type cells.

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Remark: mutagenesis experiments demonstrate that conserved amino acid residues, functionally critical in the human cystic fibrosis transmembrane conductance regulator (hCFTR), play a vital role in YCF1-mediated cadmium resistance. Remark: substitution of a serine to alanine residue in a potential protein kinase A phosphorylation site in a central region of YCF1, which displays sequence similarity to the central regulatory domain of hCFTR, also rendered YCF1 nonfunctional. Remark: the YCF1 gene of *S. cerevisiae* is an MgATP-energized, uncoupler-insensitive vacuolar membrane glutathione S-conjugate transporter. Similarity: the predicted *A. niger* protein shows strong similarity to cadmium factor (YCF1) from *S. cerevisiae*, which belongs to the ATP binding cassette (ABC) protein superfamily of membrane transporters. Title: strong similarity to cadmium resistance protein Ycf1 - *Saccharomyces cerevisiae* [putative sequencing error] putative sequencing error"

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		/inference="profile:PFAM:PF00046" /note="unnamed protein product; Function: the CUP1 gene, and its copper-dependent transcriptional activator ACE1 play a key role in mediating copper resistance in <i>S.</i> <i>cerevisiae</i> . Similarity: the predicted <i>A. niger</i> protein shows similarity to the copper homeostasis protein CUP9 from <i>S.</i> <i>cerevisiae</i> . the predicted <i>A. niger</i> protein shows strong similarity to the homeobox domain of many homeotic proteins. Title: similarity to copper homeostasis protein Cup9 - <i>Saccharomyces</i> <i>cerevisiae</i> nucleus" /citation=[26] /codon-start=1 /protein-id="CAK47212.1" /db-xref="GI:134084179" /translation="MEHAHQAFPKLCDILSLFP LHDEDAVSYPATVDPIFSLPSEL DSFSPSPSPDQATSVSPDGGGPAFTRP PQRLSV EAVRTLKSWLNHPENPYPTQEK DELAQRTSLTRAQVSNWFINARRKRKSS GYMSAR QSPSPFLSPMERWRSSPPESAAAT DDILRALADSDISAFSDSLPYTVPQYAW SSNDSS GSFVLGDASISSCGRSQSSSEKS VALSSHRPPQRPPTPLHRPSSRRHRK HIRHANR LQWTRRPYQCTFCADTFATKYDWQ RHEKALHLPVDQWRCSPEGLIIDNNGTP VCVFC QQANADEDLHLETAHNYSTCLEKPS EQRIPTRKONLRQHLKLTHRVDTFHAAM LTWRES RGRHRLSRGCGFSATFQSWQERVD HYAEHFKKHGAADMQWMDWGFEEPAQRL VENAIP PYLIGREAQTPDPWRTSDVFPMPR EEDKEDDEIPFRWDVPTALDRYFDVHRD LLAFIR EQMSGNCRPSDQMIQDRARLFAYE SDDPWNQTYADDLWCLEAVKQEAGLV"
exon	complement (91484..93088)	/locus-tag="An18g01390"
gene	<93571..>94963	/number=1
mRNA	join (<93571..93941, 93988..94242, 94300..94738, 94796..>94963)	/locus-tag="An18g01400" /locus-tag="An18g01400"
CDS	join (93571..93941, 93988..94242, 94300..94738, 94796..94963)	/locus-tag="An18g01400"
		/inference="profile:COGS:COG0477" /inference="profile:COGS:COG2271" /note="unnamed protein product;

Function: the MCT3 transporter from *Rattus norvegicus* is a proton-linked monocarboxylate transporter. it catalyzes the rapid transport across the plasma membrane of many monocarboxylates such as lactate, pyruvate, branched-chain oxo acids derived from leucine, valine and isoleucine, and the ketone bodies acetoacetate, beta-hydroxybutyrate and acetate. Similarity: the predicted *A. niger* protein shows strong similarity to the monocarboxylate transporter 3 (MCT3) of *R. norvegicus*, which belongs to the major facilitator superfamily. Title: strong similarity to monocarboxylate transporter 3 MCT3 - *Rattus norvegicus*

/citation=[44]
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 SFILDALLSRVGTAWTFRILGFITMGTGLPAAFL
 VKQRIPIPPSAFVEWRLEFRDIRFL
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 AGVVAAFNFSSALGRLTCGFASDT
 IGGLENTLFVSLLSALSMIIWFPVSTSIGPLVVF
 VIINGMANGGFFSTIPTVVGNVFG
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exon	93571..93941	/locus-tag="An18g01400" /number=1
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exon	93988..94242	/locus-tag="An18g01400" /number=2
intron	94243..94299	/locus-tag="An18g01400" /number=2
exon	94300..94738	/locus-tag="An18g01400" /number=3
intron	94739..94795	/locus-tag="An18g01400" /number=3
exon	94796..94963	/locus-tag="An18g01400" /number=4
gene	<95725..>97215	/locus-tag="An18g01410"
mRNA	join(<95725..95803, 95882..96591, 96649..>97215)	/locus-tag="An18g01410"
CDS	join(95725..95803, 95882..96591, 96649..97215)	/locus-tag="An18g01410"

		/inference="profile:PFAM:PF03663" /inference="similar to AA sequence:PIR:T52516" /note="unnamed protein product; Title: strong similarity to hypothetical protein B2J23.120 - Neurospora crassa" /codon-start=1 /protein-id="CAK47214.1" /db-xref="GI:134084181" /translation="MLLRIRWHILYTFIVVQAID YDVEDPDSIKAACHSVARQMLTHY TGNQPGDNPGNLDPFIYWWEAGAMFTALVDYWYL TSDDTWNNTTQGITWQAGPSGSF MPANQTRTEGNDQSFWFAAAMSAAERNFPDPPP SSGSPGWLAMAQAVNTQAARWDK STCNQGLRWQIFTFNNGWTYKNTISNGCFNLAA RLAKYTGNSIYADWADTVWDWTGE VGFMTDTYRFWDGADVSSGCGDWNWYIEWTYNTGV YLLGAAVMYNLTESPVWKARTEGI LNASFVFFQDDVMYERACEPVSTCQVDQSFKEY LARWMAATTQMAFFTYDLVMPKLR ASAKAAAECTCTGGELQATCGLKWTDRKWDGMDV GIQMAALEVMQSTLISRVDPPVTQ DTGTSQGNPAGGEFGPPFAPVFEGLRLEITKAD RAGAGMMTVMLSMIVIGSTGWMVY E" /locus-tag="An18g01410" /inference="protein motif:SignalP:2.0" /locus-tag="An18g01410"
sig-peptide	95725..95778	
mat-peptide	join(95779..95803, 95882..96591, 96649..97212)	
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exon	95882..96591	/locus-tag="An18g01410" /number=2
intron	96592..96648	/locus-tag="An18g01410" /number=2
exon	96649..97215	/locus-tag="An18g01410" /number=3
gene	complement(<97301..>989 81)	/locus-tag="An18g01420"
mRNA	complement(join(<97301.. .98523,98588..>98981))	/locus-tag="An18g01420"
CDS	complement(join(97301.. 98523,98588..98981))	/locus-tag="An18g01420" /codon-start=1 /product="hypothetical protein" /protein-id="CAK47215.1" /db-xref="GI:134084182" /translation="MVRGRPRFSRFRTRTSPSCAS GTRMCRNRRLQARRVMQVYSNL TCSYPIPTIMPALSVLPADILLHVISFLDHSQGV YSFLLSPSLFTLIHSNDLVNKRH YRCVRINCPDLKNAYTILLDLHDCNLANMIAL LTQATCSVSVRPPGPALSVNRNR DYSTWPCRQTLRLRIGISHTTSFASITVIEITT VSNPASTQEDAYHGKSTFIGQALT VLLIASSPNLTSLSIPPFWEYTSRFPNDPSDNH

```

HFAAKIEKYPLAKFLKHANSSHLI
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KSDLLCKVICSMKCLKELRYSVVQ
GGCYAGFAEFFDRYSLIEAILRHRTATLEVLDLEF
DDQLSQFVAVERESGVQDDAEDKS
VLKEFISLRSLSLGVSVCLWFLATGMGELGNIVLM
DHLPLQLEYLRIRGYEKGHTKTLT
NMLAGMESAREGHFALCTVQGVNEYIIPVGK"
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)
intron    complement(98524..98587 /locus-tag="An18g01420"
)
)
exon      complement(98588..98981 /locus-tag="An18g01420"
)
)
gene      complement(<100363..>10 /locus-tag="An18g01430"
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..101141,
101214..>101496))
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/inference="profile:COGS:COG1064"
/inference="profile:PFAM:PF00107"
/inference="similar to AA
sequence:PIR:S45605"
/note="unnamed protein product;
Catalytic activity: alcohol + NAD+
= aldehyde or ketone + NADH.
Pathway: alcohol dehydrogenase
ADH-T from B. stearothermophilus
is involved in glycolysis /
gluconeogenesis; fatty acid
metabolism; bile acid
biosynthesis; tyrosine metabolism;
glycerolipid metabolism. Remark:
the protein sequence of alcohol
dehydrogenase ADH-T from B.
stearothermophilus NCA1503 is
covered by patent JP04218378-A
(AC# AAR26874). Similarity: the
predicted A. niger protein shows
strong similarity to thermostable
alcohol dehydrogenase ADH-T from
B. stearothermophilus NCA1503,
which belongs to the zinc alcohol
dehydrogenase (ADH) family. Title:
strong similarity to thermostable
alcohol dehydrogenase adhT -
Bacillus stearothermophilus"
/citation=[15]
/citation=[58]
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/translation="MEYTFKVFVCGSSDGKVEKL
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```

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SDRVGMGIGGLGHLAIKLARALRYNVVALSSSE
KKREALEFGASEFYRFPNTQTPTN
HIKPVKHLLLCGSSDSDVYASVSHLPSKQNAIDH
ANIYRSLLDLVDNCTIYHISVTL
KPTPIPLVFPFGQKGIIRIQGCFITSRNLQELLEF
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96)
gene      /number=2
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join(<101875..101958, /locus-tag="An18g01440"
102203..102219,
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join(101875..101958,
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102259..102360,
102392..102399,
102621..103153,
103205..104542)

/inference="profile:COGS:COG3496"
/note="unnamed protein product;
Similarity: the predicted A. niger
protein shows local similarity to
the hypothetical protein mll8086
from M. loti. Title: strong
similarity to hypothetical protein
CAD70872.1 - Neurospora crassa"
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IKSLSKDKSVIGKPLLPITLDHT
RLSPIKNNFTFNVLEVGIVGVISCRFGRLLSIDA
KHTDEECTERSLLRLQLTYFSS
WFSFDSARYLHRGDDTSLLENLKNKFLREQNENP
AKWPYAYMLSVPRFLWVERSVMVW
WLYSESKELDAVIMEINNSFDEKRNVLKVRRT
RIYTESPEKGFEQLLDCKEEHLE
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TVSSFTFLDPVVPSSWGNRSLSNT
TTFDPSGAPRMIA RLWCKVPPIDPGKASSFQIFS
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LHSLFDLHANLQSRMLERFFREYL

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intron	102361..102391	/locus-tag="An18g01440"
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CDS	join(106231..106565, 106647..106803)	/locus-tag="An18g01450"

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 /note="unnamed protein product;
 Function: ordA of A. parasiticus
 is involved in the aflatoxin
 biosynthesis and converts
 O-methylsterigmatocystin (OMST) to
 aflatoxins B1 or G1 and converts
 dihydro-O-methylsterigmatocystin
 (DHOMST) to aflatoxins B2 or G2.
 Remark: aflatoxins comprise a
 group of polyketide-derived
 carcinogenic mycotoxins. Remark:
 it is assumed that the ORF is
 N-terminally shorter and has
 another start codon 5' to the
 predicted one ; the ORF is around
 400 amino acids shorter than most
 of the homologues cytochrome p450
 proteins. Remark: ordA of A.
 parasiticus is also called
 cytochrome p450 64, cyp64 or omst
 oxidoreductase. Similarity: the
 ORF shows similarity to several
 cytochrome P450 related proteins
 from different species. Title:
 strong similarity to
 O-methylsterigmatocystin
 oxidoreductase ordA - Aspergillus

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intron	106566..106646	
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gene	<107279..>108340	
mRNA	join(<107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..>108340)	
CDS	join(107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..108340)	/locus-tag="An18g01460"

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 /inference="profile:PFAM:PF00106"
 /note="unnamed protein product;
 Catalytic activity: cyclohexanol
 dehydrogenases convert
 cyclohexanol + NAD(+) <=>
 cyclohexanone + NADH. Function:
 chnA of A. sp. is an alcohol
 dehydrogenases proposed to
 catalyze the conversion of
 cyclohexanol to cyclohexanone (EC
 1. 1. 1. 245). Phenotype:
 cyclohexanol was detected as the
 major intermediate accumulated in
 the chnA mutant of A. sp. Remark:
 chnA of A. sp. is encoded in the
 gene cluster for cyclohexanol
 oxidation. Similarity: the ORF
 shows similarity to several
 dehydrogenases from different
 species and with various
 specificities. Title: strong
 similarity to cyclohexanol
 dehydrogenase chnA - Acinetobacter
 sp"
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exon	108151..108340	/locus-tag="An18g01460"
		/number=6
gene	<108826..>111209	/locus-tag="An18g01470"
mRNA	join(<108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960, 111135..>111209)	/locus-tag="An18g01470"
CDS	join(108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960,	/locus-tag="An18g01470"

111135..111209)

/EC-number="1.14.-.-"
 /inference="profile:COGS:COG0493"
 /note="unnamed protein product;
 Remark: aflatoxins are
 polyketide-derived secondary
 metabolites. Remark: moxY of A.
 parasiticus is expressed
 concurrently with genes involved
 in aflatoxin biosynthesis and it
 lies on one end of the cluster of
 this genes. Therefore moxY of A.
 parasiticus is presumably also
 involved in aflatoxin
 biosynthesis. Similarity: the ORF
 shows similarity to monooxygenases
 from several species and with
 different functions. Title: strong
 similarity to monooxygenase moxY
 -Aspergillus parasiticus"
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 FFPKQEEILQYIHGVADEFVSALK
 LVGHTEWEGADWQDSEQCWEVRLREIPSGRKFR
 RCRILISAVGGLTNPKHVMLOGIE
 RFQGNIVHTALWDQETAVAGKNVIVIGNGASATQ
 FIPAIADDAASINQFIRHVRKCAP
 EEQYWSLLTPEYSIGCKRRVFDNDGYLKCLHRPN
 VDIINDFVVAVEEQSIITTSQGRKF
 PADLIADVLDYGRCLRLGSLRSRSTMTGEVVMG
 VRDKNIGTVSAAYKHLRRWPWRNF
 LTFSTFSDPTLAGAIHQLSIQLKVSVVIKQASEE
 RFNTKLKSALRKTVFTNMCRSLPA
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exon	109020..109023
intron	109024..109088
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intron	109306..109376
exon	109377..109778
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exon	109841..109905
intron	109906..110159
exon	110160..110181

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CDS	111907..113460	/locus-tag="An18g01480"

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 /inference="profile:PFAM:PF00067"
 /inference="similar to AA
 sequence:UniProtKB:AB013443.1"
 /note="unnamed protein product;
 Function: eln2 of C. cinereus
 encodes a novel type of microsomal
 cytochrome P450 enzyme, with is
 involved in mushroom
 morphogenesis. Phenotype: a
 dominant mutation of the
 elongationless2 (eln2) gene of the
 mushroom C. cinereus affects
 pattern formation in the
 development of fruit body
 primordia, causing dumpy primordia
 which culminate in mature fruit
 bodies with short stipes.
 Similarity: the ORF shows
 similarity to several cytochrome
 p450 related proteins from
 different species, which have
 different cellular functions.
 Title: strong similarity to
 cytochrome p450 related protein
 eln2 - Coprinus cinereus"
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 YHPIQDLESKQLMFDLLRSNDFDA
 HFERYSGSLMFALAYGFRLLSPKGQELDRMTIQ
 GNFTYAARVGTVIVDAIPVLNLYLP

		AVVAPWKRLAEKLFKLEASVHTRHLEKGLNSEPW NWSKEFAASKHAEGMPRLDLAYNL GILVDAGFETTWTVMKIFVLAMRSDPRFVAVARK ELDEVVGEDRMPTEFDEQKLVYIQ AVVDETLRWRSMAFGGIPHAARKEDTYMGYRIK GATVIFLWRSMLTDEPWDDPLEF RPERWFEATEKEEGFRNFFGYGRRICTGRHIAR NSLELLMARILWAFDIQAPLGDDG KPVPVDDMAFDSAFVSTPEPFALFVPRSEKTK IVEREWNEKMDAVLMGQVRDSQ RALGLDVRA"
sig-peptide	111907..111957	/locus-tag="An18g01480" /inference="protein motif:SignalP:2.0"
mat-peptide	111958..113457	/locus-tag="An18g01480" /product="unnamed"
exon	111907..113460	/locus-tag="An18g01480" /number=1
gene	complement(<113565..>114733)	/locus-tag="An18g01490"
mRNA	complement(join(<113565..114153, 114210..>114733))	/locus-tag="An18g01490"
CDS	complement(join(113565..114153, 114210..114733))	/inference="profile:COGS:COG0598" /inference="profile:PFAM:PF01544" /inference="similar to AA sequence:UniProtKB:SC41293.1" /note="unnamed protein product; Function: alr2 of S. cerevisiae is an uptake transporter for inorganic cations, e. g. magnesium, which presence seems to be important for resistance to the toxic effect of aluminum. Remark: alr2 of S. cerevisiae is also called YFL050C. Similarity: the predicted ORF is 395 amino acids shorter at the N-terminus and 57 amino acids shorter at its C-terminal end than alr2 of S. cerevisiae (nearly the same is true for alr1 of S. cerevisiae). Title: strong similarity to ion transporter Alr2 -Saccharomyces cerevisiae plasma membrane" /citation=[40] /codon-start=1 /protein-id="CAK47222.1" /db-xref="GI:134084189" /translation="MSSDSTPDPRLEKPRVAVAS RLNFFTSQNLNTSIEASSIEDLCSV YRPFELLLETGAHSGLWLDITAPSEEDIEALAR FFNHLPLTTEDIKTRETREKIELF GQYYFLSLRPPRRLETDIGVRIVSHNLYAVVFRG GVLSFSFDPSSLHTSHVRQRIKEHS SHLLLTSDWICYALIDIDVDFAPPISRVENGVV TVEDSVSITRPDDMGLAQRIKFL RKEVMNIRQLHDKIDVIRSFARHCDISDTSSSQ VALYLSIDICDHVVMTIANLEQAQ

```

                                MLSRLQSKYLTQVHFDSGMRNGIASALSCLTLVL
                                ASILVPMQFITGLFGMNVRVPGKT
                                HDGDNLSLTWWFSILGFILGLTVIFAWVAKRIGLL
                                DR"
exon          complement(113565..1141 /locus-tag="An18g01490"
53)
                                /number=1
intron        complement(114154..1142 /locus-tag="An18g01490"
09)
                                /number=1
exon          complement(114210..1147 /locus-tag="An18g01490"
33)
                                /number=2
gene          complement(<115549..>11 /locus-tag="An18g01500"
6444)
mRNA          complement(join(<115549 /locus-tag="An18g01500"
..115734,
115791..116016,
116080..>116444))
CDS           complement(join(115549. /locus-tag="An18g01500"
..115734,115791..116016,
116080..116444))

                                /note="unnamed protein product;
                                Title: strong similarity to
                                hypothetical protein encoded by
                                An15g02540 - Aspergillus niger"
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                                /protein-id="CAK47223.1"
                                /db-xref="GI:134084190"
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                                FPLSLEGTKDQPFWRFPYEEELPLPVEEAEFLQI
                                ELTPDNIMWDTRALELFLDFHFD
                                CRGFAKCEYPQNPPYGVYREIGDVKFGQLLECGK
                                FNWYAVSVIDYPGENLPHIKAIVE
                                NDAIGDDKLLRGEIMTITDIMKARLRNNTLRPHI
                                VAPMLVLSLMGPRHARVLEADFDG
                                VMLNIRASGLYDFTRKNTDAVQLLTRYNLGGACG
                                QTTKKS"
exon          complement(115549..1157 /locus-tag="An18g01500"
34)
                                /number=1
intron        complement(115735..1157 /locus-tag="An18g01500"
90)
                                /number=1
exon          complement(115791..1160 /locus-tag="An18g01500"
16)
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intron        complement(116017..1160 /locus-tag="An18g01500"
79)
                                /number=2
exon          complement(116080..1164 /locus-tag="An18g01500"
44)
                                /number=3
gene          complement(<117672..>11 /locus-tag="An18g01510"
8234)
mRNA          complement(join(<117672 /locus-tag="An18g01510"
..117782,
117885..118021,
118123..>118234))
CDS           complement(join(117672. /locus-tag="An18g01510"
..117782,117885..118021,

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118123..118234))

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/feature="unnamed protein product;
Remark: the ORF is questionable
due to its suboptimal intron-exon
structure and short lenght Title:
questionable ORF"
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SGSDVGLPPFACQSLGWQTNVAVLG
PVYKGFASIAIILLICIFGQWDEDLVTRGNIIS
GVDGETLTKVLLPVLTKMRTWLKG
YHLLIGGVAVCLCVCFV"
exon      complement(117672..1177 /locus-tag="An18g01510"
82)
/number=1
intron    complement(117783..1178 /locus-tag="An18g01510"
84)
/number=1
exon      complement(117885..1180 /locus-tag="An18g01510"
21)
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intron    complement(118022..1181 /locus-tag="An18g01510"
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/number=2
exon      complement(118123..1182 /locus-tag="An18g01510"
34)
/number=3
gene      <119176..>120297 /locus-tag="An18g01520"
mRNA      <119176..>120297 /locus-tag="An18g01520"
CDS       119176..120297 /locus-tag="An18g01520"
/EC-number="1.-.-.-"
/inference="profile:COGS:COG0673"
/inference="profile:PFAM:PF01408"
/inference="similar to AA
sequence:UniProtKB:ENQUTCH.2"
/feature="unnamed protein product;
Function: due to the presence of a
putative 'zinc cluster' motif and
its low (16%) but significant
similarity with the DNA-directed
DNA polymerase of hepatitis B
virus,it was assumed that qutH of
A. nidulans is a DNA-binding
protein, which is possibly
involved in the regulation of
genes essential for the
utilisation of protocatechuic
acid. Function: due to the
similarity of the ORF to
oxidoreductases, it is here
assumed that the ORF is encoding a
protein with oxidoreductase
activity. Similarity: the ORF
shows similarity to several
oxidoreductases from different
species. Title: strong similarity
to quinic-acid utilisation gene
qutH - Aspergillus nidulans"
/citation=[10]
/codon-start=1

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/protein-id="CAK47225.1"
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/translation="MLNVIIVGAGLIGPRHAQSV
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LNTLYFPLSALLSSVPNIPHPDAAI ICTPNHHT
VPVALELISHNIIHILLEKPIISDTI
TTALPLLQAQQKYPDVKILIGHHRRFNPIYITKT
EILESGLGPIIALSGLWTLYKPA
SYFTGATEWRRDKAKGGVLSINLIHDVDLLHYLF
GPITRVYAEKTLPRGGPDGNENH
TAEEGAAITFRFASGVVGTFFVSDCAPSPWNFEA
GTGENPIIPKVGSGVGGGLYRVLS
RGSLSVPDLKRWSYDGVGEKGWNQRLQVEFEFV
DEGVFPDLQLEHFVRVLRGETPR
CDAVEGLRALVVDAVKRAMETEVEVVKVESVEEI
LARNE"
sig-peptide      119176..119226    /locus-tag="An18g01520"
                  /inference="protein
motif:SignalP:2.0"
mat-peptide      119227..120294    /locus-tag="An18g01520"
                  /product="unnamed"
exon              119176..120297    /locus-tag="An18g01520"
                  /number=1
gene              complement(<120373..>12 /locus-tag="An18g01530"
1787)
mRNA              complement(join(<120373 /locus-tag="An18g01530"
..120856,
120912..121419,
121479..121515,
121584..>121787))
CDS               complement(join(120373. /locus-tag="An18g01530"
..120856,120912..121419,
121479..121515,
121584..121787))

/note="unnamed protein product;
Function: pth11 of M. grisea is
involved in host surface
recognition for the initiation of
appressorium formation, which is
important in plant infection.
Phenotype: M. grisea pth11 mutants
are nonpathogenic due to a defect
in appressorium differentiation.
Remark: on the same contig another
ORF shows similarity to pth11 of
M. grisea, see 130cg. Similarity:
the ORF is 85 amino acids shorter
at its N-terminus and 155 amino
acids shorter at the C-terminal
end than pth11 of M. grisea.
Title: strong similarity to
integral membrane protein PTH11 -
Magnaporthe grisea"
/citation=[52]
/citation=[60]
/codon-start=1
/protein-id="CAK47226.1"
/db-xref="GI:134084193"
/translation="MAVDPAIVAIFGEPPDDIDL
TDSRVQQDNAVVFILCLAVISVV
LRFVARRVLRNLSMADDWVILALVFICTTSGLS
ISGGFYGAGKHVWAIISVTKLVTLF

```

KVSSTPHSTVVRALTSQILYIYVMVYSAVCCA
 AK
 VSILFFYRRVFMASHADLSLRIGI
 YLGFFLTLSYPIICVMTATAKCPASYFWNQFGG
 ASGTCIDTDTFFLALGIINMLNDI
 VVLLIPFPQIAKLQMNRRKKVAISGILAVGSFAC
 VASIVRIYSVDQFTKRTDVTWTLG
 PVFIWSTIEPGLSLVCACPLHPLVRLAHIKLS
 SSQDSKRSRPTNPSTPWRSRSGNA
 NGNGTFSAGRRVHVSVLSTKYTFDGDQDEEIGLTN
 HVTTSASLRKPHSIESVEREGGGS
 VDQSIMVHSSFFVQSVSNK"

exon complement(120373..120856) /locus-tag="An18g01530"

intron complement(120857..120911) /number=1 /locus-tag="An18g01530"

exon complement(120912..121419) /number=1 /locus-tag="An18g01530"

intron complement(121420..121478) /number=2 /locus-tag="An18g01530"

exon complement(121479..121515) /number=2 /locus-tag="An18g01530"

intron complement(121516..121583) /number=3 /locus-tag="An18g01530"

exon complement(121584..121787) /number=3 /locus-tag="An18g01530"

gene <122486..>123895 /number=4 /locus-tag="An18g01540"

mRNA <122486..>123895 /locus-tag="An18g01540"

CDS 122486..123895 /locus-tag="An18g01540"

/EC-number="2.3.1.-"
 /inference="similar to AA
 sequence:UniProtKB:AB014491.1"
 /note="unnamed protein product;
 Function: TRI101 of F.
 sporotrichioides conferred
 significant increased tolerance to
 the mycotoxin DAS (trichothecene
 4,15-diacetoxyscirpenol), which is
 harmful for vertebrates. Function:
 TRI101 of F. sporotrichioides
 converts isotrichodermol to
 isotrichodermin and is required
 for the modification of T-2 toxin,
 which inhibits protein synthesis
 in eukaryotes. Phenotype: TRI101
 mutants of F. sporotrichioides
 were altered in their abilities to
 synthesize T-2 toxin and
 accumulated isotrichodermol and
 small amounts of
 3,15-didecalonectrin and
 3-decalonectrin, trichothecenes.
 Title: strong similarity to
 trichothecene
 3-O-acetyltransferase TRI101 -
 Fusarium sporotrichioides"

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/citation=[48]
/citation=[53]
/citation=[56]
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/db-xref="GI:134084194"
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LGPNAEEPILVKDLRTQDTLPSYA
ELKTQHFFPVAAFNADTLCCRDIWPTDLGEHLPI
LVQANFIRGGILITWCILHMAGDG
NSFQTWMRVWAECCRRAGQVKITDPVVLPPAIFA
DREKVMRSSGRNPGRIEDHPEYVV
LPFPKPEGLPPKMLAKNHRAQVIFYFSPEALAAK
KEASPKNASEPRDVPWISTNDALS
ALLWRTVMAVQWPLETLESVNQDQESFFNIALNG
RLRTDPFVHPNTLGCFLFYIGVSM
FVHKMLTSAQLANLAVLIRQALHQVSNQHTDDVI
SLIEQLDDIRKIFPASLVDLPGFN
CILTSDWDFALYNLDWGTLLGGHIESVRAPHVGV
INGLQVVLPNPREGMEVLVGAD
GCLEKLLNDPLWMKYAVAR"
exon      122486..123895 /locus-tag="An18g01540"
          /number=1
gene      complement(<123984..>12 /locus-tag="An18g01550"
          7145)
mRNA      complement(join(<123984 /locus-tag="An18g01550"
          ..124060,
          124183..125132,
          125181..125432,
          125485..125732,
          125913..>127145))
CDS       complement(join(123984. /locus-tag="An18g01550"
          .124060,124183..125132,
          125181..125432,
          125485..125732,
          125913..127145))

/note="unnamed protein product;
Title: similarity to hypothetical
protein AAM43672.1 - Dictyostelium
discoideum"
/codon-start=1
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KGSETLVDESVRKTWQLDPGQFSL
QNPLWQQQMDDVDDAVTGLGLTAQSDEVQAELY
KLLIYEEGAFFLPHQDTEKADGMF
ATLVVCLPSKHEGGTLVASHRGWKIAWSTASSSE
FSFSWAAWYADVIHEVRPVTSGYR
VALVYNLIHRPLVGLGISGVQTDKLTLLLESWVS
DCSNGQSDHSAWDHHINGDCPPA
LVVYVLEHQYTVVVELSFDRLLKGVQVRFGEQKAC
QGLDFDLYLANIEKTRMGVDGRI
GNSYWKAHNALEDVLGGNQKFLSVVDASGSVEVG
RLPFHGKLLIQEDFFSNRLPDDEK
YQGFTEGNEAAKATRVYRATLFSEQPDNALTKRNL
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AIDVDDVILFCQTLVSLEGTMSSSEITQTAKVLA

```

KHGLEAIRLALERVFDQKPHGPSL
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 LTPLPQEGLFERIIPFLETKIERTACLKGFVSV
 YVYSRRGKFDQDAVDAMLKNLLPK
 FFRGRFVQYKHTSNSGLEFAANCRPTKHTTSIRI
 DPKTVVGLIKLGDVMDVDNTALEFH
 ALTEYTLVDQARDMPDVFTDFLLPVANGVCENVI
 TSGGPSTNSERRFVKHILNKYITG
 YVLPAPLVPPDWKGRSCILRCYTCASLDTFIED
 PAVRTRKRVHMGNDMEHFDRLDD
 FFFTKTVVGPVGMQMLRIWKTAMMLVSQLHAWN
 KRARDAKAQLDQLDKHRSLEKILG
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 SVVPNITLYRQIDDEYMSACTDEC TNAST"

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intron	complement(124061..124182)	/locus-tag="An18g01550"
		/number=1
exon	complement(124183..125132)	/locus-tag="An18g01550"
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intron	complement(125133..125180)	/locus-tag="An18g01550"
		/number=2
exon	complement(125181..125432)	/locus-tag="An18g01550"
		/number=3
intron	complement(125433..125484)	/locus-tag="An18g01550"
		/number=3
exon	complement(125485..125732)	/locus-tag="An18g01550"
		/number=4
intron	complement(125733..125912)	/locus-tag="An18g01550"
		/number=4
exon	complement(125913..127145)	/locus-tag="An18g01550"
		/number=5
gene	<127862..>129230	/locus-tag="An18g01560"
mRNA	join(<127862..127973, 128149..128238, 128310..128432, 128566..128684, 128777..128854, 128935..129026, 129125..>129230)	/locus-tag="An18g01560"
CDS	join(127862..127973, 128149..128238, 128310..128432, 128566..128684, 128777..128854, 128935..129026, 129125..129230)	/locus-tag="An18g01560"

/note="unnamed protein product;
 Remark: the ORF is questionable
 due to its suboptimal intron-exon
 structure. Title: questionable
 ORF"

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		/db-xref="GI:134084196"
		/translation="MQHAAGKPAADDMRNKALHA ISLGQAFHGSSPGRAVSAKERTSI VNPAQMTADMVGVRFLPHWDGWSGVHYSNRLFL DWRSVASSGDEGKSEFFPDGVWTGQ ALESIANMQLRGLPLRVPGDFRQFHPPPLFLSLAK DFFIPVDVANSITAKPETIPGQS LSAISPFPLSCGMRGTNAVSGPDLPSGKSCASHQ RVSASTLAFRTGGSRIPGYRTEEQ MATPCHEPWLSSRRARRIPNVY"
exon	127862..127973	/locus-tag="An18g01560"
		/number=1
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intron	128239..128309	/locus-tag="An18g01560"
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		/number=3
exon	128566..128684	/locus-tag="An18g01560"
		/number=4
intron	128685..128776	/locus-tag="An18g01560"
		/number=4
exon	128777..128854	/locus-tag="An18g01560"
		/number=5
intron	128855..128934	/locus-tag="An18g01560"
		/number=5
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		/number=6
intron	129027..129124	/locus-tag="An18g01560"
		/number=6
exon	129125..129230	/locus-tag="An18g01560"
		/number=7
gene	<129407..>130916	/locus-tag="An18g01570"
mRNA	join(<129407..129556, 129604..129720, 129768..129958, 130008..130130, 130176..130256, 130321..130729, 130866..>130916)	/locus-tag="An18g01570"
CDS	join(129407..129556, 129604..129720, 129768..129958, 130008..130130, 130176..130256, 130321..130729, 130866..130916)	/locus-tag="An18g01570"

/note="unnamed protein product;
Function: pth11 of M. grisea pth11
is involved in host surface
recognition for the initiation of
appressorium formation, which is
important in plant infection.
Phenotype: M. grisea pth11 mutants
are nonpathogenic due to a defect
in appressorium differentiation.

Remark: on the same contig another ORF shows strong similarity to pth11 of *M. grisea*, see 160wg. Similarity: the ORF is 92 amino acids shorter at the N-terminal end and 165 amino acid its C-terminus than pth11 of *M. grisea*. Title: similarity to integral membrane protein PTH11 - Magnaporthe grisea"

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IPIKLSISWMLIRVAEGRKAYLYAQYVVIVVFWL
MNIIALIFILINCPVDAANTEL
LKQGGHCQPSYVLADVYYACTAVNILTQWVIALM
PVPLLWNVQLNRNTKISIVGLMGL
GIFASMSACVRLKYITVALTSQSNLYSVTNVVIW
GFTENALGMIVGNVATLRPLRIL
RDRKTSSNNKYNRSGYISSQRTGPNMYSRNYEL
AEQKGHTNQITTTSMADHTRRFSQ
MSDGDSSQKQILAGGTTPPGDTDLKKELNDSLQQLQ
FSKQA"

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mat-peptide	join(129494..129556, 129604..129720, 129768..129958, 130008..130130, 130176..130256, 130321..130729, 130866..130913)	/locus-tag="An18g01570"
exon	129407..129556	/product="unnamed" /locus-tag="An18g01570"
intron	129557..129603	/number=1 /locus-tag="An18g01570"
exon	129604..129720	/number=1 /locus-tag="An18g01570"
intron	129721..129767	/number=2 /locus-tag="An18g01570"
exon	129768..129958	/number=2 /locus-tag="An18g01570"
intron	129959..130007	/number=3 /locus-tag="An18g01570"
exon	130008..130130	/number=3 /locus-tag="An18g01570"
intron	130131..130175	/number=4 /locus-tag="An18g01570"
exon	130176..130256	/number=4 /locus-tag="An18g01570"
intron	130257..130320	/number=5 /locus-tag="An18g01570"
exon	130321..130729	/number=5 /locus-tag="An18g01570"
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exon         130866..130916      /locus-tag="An18g01570"
                                     /number=7
gene         complement(<131646..>13 /locus-tag="An18g01580"
2375)
mRNA         complement(join(<131646 /locus-tag="An18g01580"
..132295,
132363..>132375))
CDS          complement(join(131646. /locus-tag="An18g01580"
.132295,
132363..132375))

                                     /EC-number="4.2.1.1"
                                     /inference="profile:COGS:COG0288"
                                     /inference="profile:PFAM:PF00484"
                                     /inference="similar to AA
sequence:UniProtKB:AB040135.1"
                                     /note="unnamed protein product;
Catalytic activity: pcal of P.
purpureum converts H(2)CO(3) <=>
CO(2) + H(2)O with the usage of
zinc as cofactor. Function:
carbonic anhydrases catalyze the
reversible hydration of carbon
dioxide. Remark: an alternate name
for pcal of P. purpureum is
gtppcal. Similarity: the ORF shows
similarity to several carbonic
anhydrases from different species
and with various cellular
functions. Title: strong
similarity to carbonic anhydrase
pcal - Porphyridium purpureum"
                                     /citation=[32]
                                     /citation=[62]
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NIANVVNAADVNCAAVVEYAVLHL
KVKHVVVCGHTCCGGVGAVLAAPKGERDGEDGEK
SVLDAWLSSLKRVRDRYASELEGI
HGEYERGVRLVELNVLEGVRLMAMGVVREAVEK
GEVEVHGAVYNVGCGVVRELELV KL"

exon         complement(131646..1322 /locus-tag="An18g01580"
95)
                                     /number=1
intron      complement(132296..1323 /locus-tag="An18g01580"
62)
                                     /number=1
exon         complement(132363..1323 /locus-tag="An18g01580"
75)
                                     /number=2
gene         complement(<133082..>13 /locus-tag="An18g01590"
5202)
mRNA         complement(join(<133082 /locus-tag="An18g01590"
..133214,
133277..134939,
135000..135045,
135113..>135202))

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CDS      complement(join(133082..133214,133277..134939,
                        135000..135045,
                        135113..135202))
                        /locus-tag="An18g01590"
                        /EC-number="2.3.1.7"
                        /inference="profile:PFAM:PF00755"
                        /inference="similar to AA
                        sequence:PIR:S68958"
                        /note="unnamed protein product;
                        Catalytic activity: cat2 of C.
                        tropicalis catalyses acetyl-CoA +
                        carnitine <=> CoA +
                        O-acetylcarnitine. Function: cat2
                        of C. tropicalis is specific for
                        the acetylation of short chain
                        fatty acids and may also be
                        involved in the transport of
                        acetyl-CoA into mitochondria.
                        Similarity: the ORF overlaps with
                        A. niger EST EMBEST:BE760390.
                        Title: strong similarity to
                        carnitine O-acetyltransferase cat2
                        - Candida tropicalis inner
                        membrane"
                        /codon-start=1
                        /protein-id="CAK47232.1"
                        /db-xref="GI:134084199"
                        /translation="MFAASSRNRLSTLPRTRLSP
                        ANSLARSAVTPIMAPRRKASSVP
                        EGYKEDLSKGNMLRFEDSLRPLVPSLEETGRRY
                        LKSVHALVSEAEYERTKKAVEAFV
                        RPPGEGEPLQERLLARAADPKIKNWLLLEWNNHAA
                        YLGYRDEVPYVYSYFYSDRDRAR
                        RDPAKRAASVATAALEFKRQVDDGSLPEYMRGQ
                        PMAMSTYQYMFNCCRIPGDSVDYP
                        QKFPAQDNEHIVVVRKNQFFKVPLTVNGKRLNNS
                        ELQRQFERIYEVAQFAPAVGVLTV
                        ANRDLWADARKKLLAAHPANEQALRDIESSGFLV
                        CLDNATFPVTLEERAHQYWHGDGTN
                        RWFDPKPLQFIINDNGTAGFMGEHSMMDGSPTHRM
                        NDHLNLIIFNHKIDLSEKPVRSDL
                        PDPRPITFHLDPVLLEAIDANKHRQQISSHEL
                        RVQAYQGYGKGLIKFKCSPDAYV
                        QMIQLAYFKMYGKNRPTYESASTRKQFQGRTE
                        TRTVSDSVAFCKAISDPFVPRE
                        AVRLLRSALAAHTKYTAEASDGRGVDRHLFGLKK
                        LLREGKLPALYEDPAFAYSSSWY
                        LSTSLSSEFFNGYGSQVDDGFGIAYMINENS
                        LNFNIVCKRLGAERMSYLLNEAAS
                        DMRDMLMPDLAAQSEKAKM"
exon      complement(133082..133214) /locus-tag="An18g01590"
intron    complement(133215..133276) /number=1
exon      complement(133277..134939) /locus-tag="An18g01590"
intron    complement(134940..134999) /number=2

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exon      complement(135000..1350 /locus-tag="An18g01590"
45)
                                     /number=3
intron    complement(135046..1351 /locus-tag="An18g01590"
12)
                                     /number=3
exon      complement(135113..1352 /locus-tag="An18g01590"
02)
                                     /number=4
gene      complement(<135940..>13 /locus-tag="An18g01600"
7166)
mRNA      complement(join(<135940 /locus-tag="An18g01600"
..136119,
136175..136476,
136534..136864,
136972..>137166))
CDS       complement(join(135940. /locus-tag="An18g01600"
.136119,136175..136476,
136534..136864,
136972..137166))

/inference="profile:COGS:COG0515"
/note="unnamed protein product;
Function: srpk2 was first found to
mediate the interaction and
localization of pre-mRNA splicing
factors by phosphorylating the SR
(serine/arginine-rich) family of
splicing factors and therefore
probably controls the activity of
splicing. Phenotype:
overexpression of srpk2 in M.
musculus causes disassembly of
cotransfected SF2/ASF and
endogenous SC35. Similarity: the
ORF shows similarity to several
protein kinases from different
species and with various
specificity. Title: strong
similarity to serine/arginine-rich
protein-specific kinase srpk2 -
Mus musculus deleted EC-number
2.7.1.37"
/citation=[41]
/codon-start=1
/protein-id="CAK47233.1"
/db-xref="GI:134084200"
/translation="MASLLKWIRASIHPRRAPLP
PRRFPTTGFTIIPASTILEEEHFN
SFTNGHYYPVNIIGDVFASKYQMIIRSHRYVTLKIY
TRDESHTEEFKTYQHISQANPSHP
GYGYVRTALDTFIIPRPGGDHPCLVQQPMWDSFT
DLLFRNPRHRFTEDLLKAGLMQVF
LALDYLHTECRVVHTDIKGGNILEIRDNSLMEA
FTAGEMERFSSRKLADGVVPYASR
RFGLPISFGRAVLSDFGSAVRGDES RDHDAQPAV
YRSPEVMLQVGWSYLVDIWNVGVM
IWDLFEGKHM FYGEDPDGKGYSTRAHLAEVIGLL
GHPPLDLLQRGKRSEHFFTEDGML S"

exon      complement(135940..1361 /locus-tag="An18g01600"
19)
                                     /number=1
intron    complement(136120..1361 /locus-tag="An18g01600"

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74)
exon      complement(136175..1364 /number=1
76)      /locus-tag="An18g01600"

intron    complement(136477..1365 /number=2
33)      /locus-tag="An18g01600"

exon      complement(136534..1368 /number=2
64)      /locus-tag="An18g01600"

intron    complement(136865..1369 /number=3
71)      /locus-tag="An18g01600"

exon      complement(136972..1371 /number=3
66)      /locus-tag="An18g01600"

gene      complement(<138020..>14 /number=4
0061)    /locus-tag="An18g01610"

mRNA      complement(join(<138020 /locus-tag="An18g01610"
..139287,
139338..139723,
139790..>140061))

CDS       complement(join(138020. /locus-tag="An18g01610"
.139287,139338..139723,
139790..140061))

/inference="similar to AA
sequence:PIR:A40711"
/note="unnamed protein product;
Function: srb4 of S. cerevisiae is
a component of the multi
subunit complex, which binds to RNA
polymerase II and is essential for
efficient establishment of the
transcription initiation
apparatus. Phenotype: the S.
cerevisiae srb4 the null mutant is
inviable and srb4 mutants display
global defects in mRNA synthesis.
Remark: an alternate name for srb4
of S. cerevisiae is YER022w.
Title: strong similarity to RNA
polymerase II suppressor protein
Srb4 - Saccharomyces cerevisiae
nucleus"
/citation=[22]
/codon-start=1
/protein-id="CAK47234.1"
/db-xref="GI:134084201"
/translation="MSDSFSLPLRPLTEKPDPRD
TLPIEIAQINARWGSFRDVTNEETL
LAKIEEDKNRDPWEEDEDEKLAEDVDSTERLET
LYKRRAEILQFAMQAHMEALFALD
FVSLLLSKHTPRQAETSMSAFLKQVAPLGLSLNAE
IVEPPPKSEAAVQDVKTIVSRGWRA
QNFNAAANKLLNSATRLLEEVEASETKYNDVFLAV
KEKGWKVCRPLPRETALGVQYGFEL
EATPIFRDRGLAALRRADNGSLILDKGLAPQKTR
TVRVRVKHRGQLTGCSKMPDPIDP
AASVERRILQARDTVYEEELFHELMREARIMGSH
GVTTTRQNLVRLPISEDQEIILLDLV
DADRETPEDEKDIESTEHVDVLANGLSHSIRILLAY

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AHRQNLRRRTQPPPLSQKRRLLTP
 EYQLLRPMAYLQHSSHVRWLESFMNDIYRVLRA
 AGIERDFHVPFASVSLPKVQAVP
 KVESLVQQFLMPFFESTFSGHLITPQSSFRVKIRT
 NPVSPPFGTHTYDISIDLPHHPEVQ
 PPGRVGLQNEAAAALMHFVKLDIVSAIALQGSKT
 TKNTTKKEGAEGTLTWEAAYPHHG
 ELLAFSTAGQSKKLIKISLSREELKVETFSLRGLE
 GFGRSGGPKAPSLQSQTWTATQTD
 SKPGLMDFVAEVSREQS"

exon	complement(138020..139287)	/locus-tag="An18g01610"
		/number=1
intron	complement(139288..139337)	/locus-tag="An18g01610"
		/number=1
exon	complement(139338..139723)	/locus-tag="An18g01610"
		/number=2
intron	complement(139724..139789)	/locus-tag="An18g01610"
		/number=2
exon	complement(139790..140061)	/locus-tag="An18g01610"
		/number=3
gene	complement(<141613..>143279)	/locus-tag="An18g01620"
mRNA	complement(join(<141613..142684,142735..>143279))	/locus-tag="An18g01620"
CDS	complement(join(141613..142684,142735..143279))	

/EC-number="5.2.1.5"
 /inference="profile:COGS:COG4716"
 /note="unnamed protein product;
 Catalytic activity: linoleate
 isomerases catalyze the
 isomerisation of
 9-cis,12-cis-octadecadienoate <=>
 9-cis,11-trans-octadecadienoate.
 Function: linoleate isomerase of
 patent W09932604-A1 is used to
 produce conjugated
 linoleic/linolenic acid (CLA) from
 oils such as sunflower oil,
 safflower oil, corn oil, linseed
 oil, etc. Similarity: the ORF
 shows strong similarity to
 myosin-crossreactive antigen,
 which could induce autoimmune
 reactions in vertebrates. Title:
 strong similarity to linoleate
 isomerase from patent W09932604-A1
 - Lactobacillus reuteri"
 /codon-start=1
 /protein-id="CAK47235.1"
 /db-xref="GI:134084202"
 /translation="MNRGNGLPKRDPKTTQAWLIGSGISLAGAVHLIHDAGVPAANI
 HILDVHSHAGGVIKSCGDARSGVLYTGSPLYFH
 DRCVEHLLSLVPSVDDPKQSLSDS

IKELDRATSPKKKSAPTRLIKHGDKGPECLYSKHL
 QIGPKYRMELIKMLENERILGEK
 AIQDAFDEAFFKTNFWTWATTFALQPWHSLVEF
 RRCLCKHLAEIERLNDVKALDRTK
 YTIYESVIMPIESYLKSGQGVDFHNAKVTNLQIN
 PKEAQTIVSGIIIKDNGEQKTEIV
 RPEDLVMVTLGSTTSATERGSNDKAPAAPPQHSHK
 EFLDDDWALWIDLMOASTIDYGNFF
 NFHNNDQSTLESFTVTLRDSDFMERYEKLNNK
 PGTGALLSFSDSNWGLSISVPRQP
 VCSQDPSSVDVFWGYGLHPEKTGNFVHKPMCHCS
 GKEILTIVLSQLGMPVDDMLANSI
 TNPVLMFMATAPLMPRRHDYRPEVIPPQSRNLAL
 VGQYVEIQDDTTLSMEYSVRGAQM
 AVFSAMKLNKHPPKIERHLLSVFDLLGGA"

exon complement(141613..1426 /locus-tag="An18g01620"
 84)

intron complement(142685..1427 /locus-tag="An18g01620"
 34)

exon complement(142735..1432 /locus-tag="An18g01620"
 79)

gene <144032..>145578 /number=2
 mRNA join(<144032..144169, /locus-tag="An18g01630"
 144230..145373, /locus-tag="An18g01630"
 145427..>145578)

CDS join(144032..144169, /locus-tag="An18g01630"
 144230..145373,
 145427..145578)

/EC-number="1.5.3.-"
 /inference="profile:COGS:COG0277"
 /inference="profile:PFAM:PF01565"
 /note="unnamed protein product;
 Catalytic activity: HDNO of A.
 oxidans catalyses
 (D)-6-hydroxynicotine + H(2)O +
 O(2) =
 1-(6-hydroxypyrid-3-yl)-4-(methyla
 mino)butan-1-one + H(2)O(2).
 Induction: HDNO of A. oxidans
 requires FAD in the enzymatic
 assay for maximal enzyme activity.
 Similarity: the ORF shows
 similarity to several
 FAD-dependent oxygenases from
 different species and with various
 specificity. Title: strong
 similarity to 6-hydroxy-D-nicotine
 oxidase 6-HDNO - Arthrobacter
 oxidans"
 /citation=[4]
 /codon-start=1
 /protein-id="CAK47236.1"
 /db-xref="GI:134084203"
 /translation="MPFLSFARALELRRQLEGTR
 AEVVICGSDDYATSIRRWSDTCEK
 EAGAVVRVTSTSEVAEVVRFCRKNHIDFVVEAGG
 HSTTGASSHHGGVVISMARMCKVL
 TDPASETVCVQGGANWDMVNHSTAPYGLAVVGAT
 ASHSGVGGSALGGGFGWLTDQHGL

		IADQLLSVKMVLADGSIVEASDEDNQDLFWAVRG AGQAFGVATEFVFAHKVDRFRFG GLVYYDVKLPLMLVSFANEFDKRQDPKSGGFFFGF AAPREIGHMVVLAVLFYDGSAYDG EAFPEPILNPPLINRAAMKSYIEMNSIANVDPV PEGKRSIGGANIMPLETSLQLNL YSQFKEAMNTYPRMEDSALVFELLPYTKAVQVPI KETACANRGPIYNVGLILCWHDS LDAKMHALQRSISKILEAQRDITDDHAVVYPNL AGHDVSAEKLFGANLPRQLKLRK YDPHNVFRKWHDLAPARSHVEQTDKP"
exon	144032..144169	/locus-tag="An18g01630" /number=1
intron	144170..144229	/locus-tag="An18g01630" /number=1
exon	144230..145373	/locus-tag="An18g01630" /number=2
intron	145374..145426	/locus-tag="An18g01630" /number=2
exon	145427..145578	/locus-tag="An18g01630" /number=3
gene	<146433..>148685	/locus-tag="An18g01640"
mRNA	join(<146433..146489, 146546..146952, 146998..147273, 147331..147795, 147845..147954, 148006..>148685)	/locus-tag="An18g01640"
CDS	join(146433..146489, 146546..146952, 146998..147273, 147331..147795, 147845..147954, 148006..148685)	/locus-tag="An18g01640"

/EC-number="2.4.1.-"
 /inference="profile:COGS:COG0438"
 /inference="similar to AA
 sequence:PIR:T00130"
 /note="unnamed protein product;
 Function: TSase of G. frondosa
 catalyzes the trehalose synthesis
 from alpha-D-glucose 1-phosphate
 and D-glucose. Similarity: the ORF
 shows similarity to a
 clock-controlled gene (ccgs) of N.
 crassa with unknown function.
 Title: strong similarity to
 trehalose synthase TSase - Grifola
 frondosa"
 /citation=[47]
 /citation=[49]
 /codon-start=1
 /protein-id="CAK47237.1"
 /db-xref="GI:134084204"
 /translation="MSSARSPFDAESWSGKPLNV
 IYAGITELVCNNSSGRVAIAIRNL
 TDLVDFLVCTWHALRPNVSDYATDIIAELKDYR
 EKNTEKIIISALHQSLVYRCPSLC
 SRLWSELDIVPLVLEHKDRERRHDDQGLATFAG
 WNKELDERADSMVRKCIKRSFGIG
 HVLHNHINFDSVDDVDRGYHVHLANAKDYKTV
 FATWSMAQCFAQDLRERREKVAFF


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SMTCCQKPDVPTRHLSRFTKSLGVRIKWFPKP
RPGMIPLIRKMQDTLEGQGDPLSD
ITINDELLILDFAYANARRYWLCENGPLRPRAEG
GVDVVIIDSAPLLTLAILSKQQDP
ERPVI FESSLQPGVSLSGTSSPQSRWDFIRTR
LTHVDLVVSLLPKELAPRIMPEEN
VGYSFSVDQLDGQNKPLTDWDVGFYGREFSSLC
RTLQMSIIRYP EEQYILHLSQFRP
GDGTLCLLHSYQKFCDAYTKEHFGRQVPKLLICH
RGPFRTPESTVIFYDAAMSQIDSSE
TLSTSVCIIPIGAVDQMNALLTNARALVQLSTL
HGVP EMLLAAIQKGTPIAVREAE
LFPFVHESENAILVDKGDEEGIARCFSRIFSVDE
VRQEGGDAGFRKLSDSNTTVGNV
CWLYLASKMSRGDKFEPGRADIYKLAREEAGYNE
CDWHAV"
exon      146433..146489      /locus-tag="An18g01640"
                                     /number=1
intron    146490..146545      /locus-tag="An18g01640"
                                     /number=1
exon      146546..146952      /locus-tag="An18g01640"
                                     /number=2
intron    146953..146997      /locus-tag="An18g01640"
                                     /number=2
exon      146998..147273      /locus-tag="An18g01640"
                                     /number=3
intron    147274..147330      /locus-tag="An18g01640"
                                     /number=3
exon      147331..147795      /locus-tag="An18g01640"
                                     /number=4
intron    147796..147844      /locus-tag="An18g01640"
                                     /number=4
exon      147845..147954      /locus-tag="An18g01640"
                                     /number=5
intron    147955..148005      /locus-tag="An18g01640"
                                     /number=5
exon      148006..148685      /locus-tag="An18g01640"
                                     /number=6
gene      complement(149158..149230) /gene="tRNA-Lys (CTT)"
                                     /locus-tag="An18e01650"
tRNA      complement(149158..149230) /gene="tRNA-Lys (CTT)"
                                     /locus-tag="An18e01650"
                                     /product="tRNA-Lys"
                                     /inference="profile:tRNAscan:1.4"
                                     /note="codon recognized: AAG"
gene      <149921..>150603      /locus-tag="An18g01660"
mRNA      join(<149921..149936,150144..150502,150577..>150603) /locus-tag="An18g01660"
CDS       join(149921..149936,150144..150502,150577..150603) /locus-tag="An18g01660"
                                     /note="unnamed protein product;
                                     Remark: the ORF is questionable
                                     due to its suboptimal intron-exon
                                     structure. Similarity: the ORF
                                     overlaps with the 5' region of the
                                     A. niger pfkA gene. Title:
                                     questionable ORF"
                                     /codon-start=1

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		/protein-id="CAK47238.1"
		/db-xref="GI:134084205"
		/translation="MKETESGDIRCFQDCKRKWA EEDIPCQHPSRICPLQRAARSPGR SAFDEHLALSPADQLSPQWVAVYSVQSTFPSNER GYLYSGAVTAGVSDVLVAHTRFFS PAPALLFSPTLQTQVISAFPPQALLIPNNC"
exon	149921..149936	/locus-tag="An18g01660"
		/number=1
intron	149937..150143	/locus-tag="An18g01660"
		/number=1
exon	150144..150502	/locus-tag="An18g01660"
		/number=2
intron	150503..150576	/locus-tag="An18g01660"
		/number=2
exon	150577..150603	/locus-tag="An18g01660"
		/number=3
gene	<150631..>153085	/gene="pfkA"
		/locus-tag="An18g01670"
mRNA	join(<150631..151371, 151428..151889, 151937..>153085)	/gene="pfkA"
CDS	join(150631..151371, 151428..151889, 151937..153085)	/locus-tag="An18g01670"
		/gene="pfkA"
		/locus-tag="An18g01670"
		/EC-number="2.7.1.11"
		/inference="profile:COGS:COG0205"
		/inference="profile:PFAM:PF00365"
		/inference="similar to AA sequence:SWISSPROT:K6PF.ASPNG"
		/note="Catalytic activity: pfkA of A. niger is catalysing ATP + D-fructose 6-phosphate <=> ADP + D-fructose 1,6-bisphosphate. Function: pfkA of A. niger is active in a key control step of glycolysis. Gene-ID: pfkA Similarity: the ORF overlaps with the sequence of entry EMBL:ANPFKA (A. niger pfkA gene) cytoplasm"
		/citation=[1]
		/citation=[5]
		/citation=[21]
		/citation=[35]
		/codon-start=1
		/product="6-phosphofructokinase pfkA-Aspergillus niger"
		/protein-id="CAK47239.1"
		/db-xref="GI:134084206"
		/db-xref="InterPro:IPR000023"
		/db-xref="InterPro:IPR009161"
		/translation="MAPPPQAPVQPPKRRRIGVLT SGGDAPGMNGVVRVAVVRMAIHSDC EAFVAYEGYEGLVNGDMMIRQLHWEDVVRGWSRG GTLIGSARCMTFRFRPGRRLRAAKN MVLRGIDALVVCVGGDGLTGADVFRSEWPGLLKE LVEVGELTEEQVKPYQILNIVGLV GSDINDMSGTDATIGCYSSLTRICDAVDDVFDTA FSHQRGFEVIEVMGRHCGWLALMSA ISTGADWLFVPEMPPKDGVWEDDMCAIITKNRKE"

		GKRRITIVIVAEGAQRHLNKKISS KIKDILTERLNLDRVTVLGHTQRGGAACAYDRW LSTLQGVAVRAVLDMKPEAPSPV ITIRENKILRMLPMDAVQHTKTVTKKHIQNEFAE AMALRDSEFKYHFSYINTSTPDH PKLLLPENKRMIRIGIIHVGAPEGGMNQATRAAVA YCLTRGHTPLAIHNGFPGLCRHYD DTPICSVREVAWQESDAWVNEGSDIGTNRGLPG DDLATTAKSFFKKFGFDALFVVGGF EAFYAVSQLRQAREKYPEFKIPMTVLPATISNNV PGTEYSLGSDTCLNTLIDFCDAIR QSASSRRRVFVIETQGGKSGYIATTAGLSVGAV AVYIPEEGIDIKMLARDIDFLRDN FARDKGANRAGKII LRNECASSTYTTQVADMIC EAKGRFESRAAVPGHFQGGKPS PMDRIRALRMAKCMHLHESYAGKSADEIAADEL SASVIGIKGSQVLFSPMGGETGLE ATETDWARRRPKTEFWLELQDTVNILSGRASVNN ATWSCYENA"
exon	150631..151371	/gene="pfkA" /locus-tag="An18g01670" /number=1
intron	151372..151427	/gene="pfkA" /locus-tag="An18g01670" /number=1
exon	151428..151889	/gene="pfkA" /locus-tag="An18g01670" /number=2
intron	151890..151936	/gene="pfkA" /locus-tag="An18g01670" /number=2
exon	151937..153085	/gene="pfkA" /locus-tag="An18g01670" /number=3
gene	complement(<153410..>154508)	/locus-tag="An18g01680"
mRNA	complement(join(<153410..153429, 153509..>154508))	/locus-tag="An18g01680"
CDS	complement(join(153410..153429, 153509..154508))	/locus-tag="An18g01680"

/EC-number="1.6.-.-"
 /inference="profile:COGS:COG0492"
 /inference="profile:PFAM:PF00070"
 /inference="similar to AA
 sequence:UniProtKB:AF281147.1"
 /note="unnamed protein product;
 Catalytic activity: NADH
 dehydrogenases catalyse NADH +
 acceptor <=> NAD(+) + reduced
 acceptor. Function: ndh of P.
 fluorescens is involved in
 colonization of this bacterium.
 Phenotype: in an oxygen-poor
 medium mutant PCL1201 of P.
 fluorescens, which carries a
 mutation in the ndh gene showed a
 decreased growth rate. Remark: the
 sequence of the database entry
 EMBL:ANPFKA (A. niger pfkA gene)
 overlaps with the ORF due a

probably wrong number of 4658 bp
for the coding sequence of the A.
niger protein, which is encoded
3'. Similarity: the ORF is 112
amino acids shorter at its
C-terminal end than ndh of P.
fluorescens. Title: similarity to
NADH dehydrogenase II ndh
-Pseudomonas fluorescens
localisation:mitochondrion"
/citation=[46]
/codon-start=1
/protein-id="CAK4/240.1"
/db-xref="GI:13408420/"
/translation="MTTDKTIITPIIGASFAGLT
TAHSLLSHFTTNKSKGIKIKILLI
NPTPNFYWAIAAPRILAKPTAFSESQYLIPIADG
FTKYSPEVFELGRATSLDFENK
LLQVEESTTNNINKALREIKYDYLVIASGSTPSA
SSSSPLFPGETETENKDKARKEVI
YPFKLSPTSTSTITETIQSAQHTISTSKKITIIG
AGPIGVELAGELADLTSSASKEK
KDITLISSTPRILPVLKESASGTATSLTSGKVR
VLNTKVISVSASKEGGGGYELKF
ENGETMDTDIYIPTIGVLPNSSYIPGEVLDEKGW
VRVDSELKVVGVDGVYAAGDVTDL LGRGG"
/locus-tag="An18g01680"

sig-peptide complement(154443..1545
08)
/inference="protein
motif:SignalP:2.0"

mat-peptide complement(join(153413.
.153429,
153509..154442))
/locus-tag="An18g01680"

exon complement(153410..1534
29)
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/locus-tag="An18g01680"

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/note="unnamed protein product;
Function: qutD of E. nidulans is
involved in quinic acid transport
with similarity to the maltose
transport protein MAL61.
Phenotype: mutations in the qutD
gene of A. nidulans cause the loss
of ability to grow upon quinic
acid as sole carbon source in
media at normal pH 6.5 and
failure to induce three enzyme
activities specifically required
for metabolism to protocatechuic
acid. Similarity: the ORF overlaps
with A. niger EST
EMBL:BE759752. Title: strong
similarity to quinate transport
protein qutD - Aspergillus
nidulans"
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 /note="unnamed protein product;
 Function: CaMDR1 of C. albicans
 the confers insensitivity to the
 anti-mitotic drug, benomyl, and to
 the dihydrofolate reductase
 inhibitor, methotrexate. Remark:

seven different mutant alleles of CaMDR1 from *C. albicans* showed distinct drug resistance profiles. Similarity: the ORF shows similarity to several major facilitator proteins from different species. Title: strong similarity to benomyl/methotrexate resistance protein MDR1 - *Candida albicans* plasma membrane"

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CDS	complement(162686..>163666)	/locus-tag="An18g01730"

/note="unnamed protein product;
Remark: the ORF is N-terminally truncated due to contig border.
Title: strong similarity to hypothetical protein encoded by An12g00980 - *Aspergillus niger* [truncated ORF]"


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LOCUS (LOC): AM270325 GenBank (R)
 GenBank ACC. NO. (GBN): AM270325
 GenBank VERSION (VER): AM270325.1 GI:134081809
 CAS REGISTRY NO. (RN): 928583-76-0
 SEQUENCE LENGTH (SQL): 226503
 MOLECULE TYPE (CI): DNA; linear
 DIVISION CODE (CI): Plants, fungi, algae
 DATE (DATE): 24 Mar 2007
 DEFINITION (DEF): *Aspergillus niger* contig An14c0180, complete genome.
 SOURCE: *Aspergillus niger*
 ORGANISM (ORGN): *Aspergillus niger*
 Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic
 Trichocomaceae; *Aspergillus*
 REFERENCE: 1 (bases 23835 to 25756)
 AUTHOR (AU): Jones, S.W.; Luk, K.C.
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 REFERENCE: 2 (bases 16557 to 19301)
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 AUTHOR (AU): Tobias, J.W.; Varshavsky, A.
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AUTHOR (AU): Russo,M.W.; Sevetson,B.R.; Milbrandt,J.
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 REFERENCE: 40 (bases 65395 to 67116)
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 AUTHOR (AU): Wood,K.W.; Sakowicz,R.; Goldstein,L.S.; Cleveland,D.W.
 TITLE (TI): CENP-E is a plus end-directed kinetochore motor required for metaphase chromosome alignment
 JOURNAL (SO): Cell, 91 (3), 357-366 (1997)
 OTHER SOURCE (OS): CA 128:45048
 REFERENCE: 42 (bases 16557 to 19301)
 AUTHOR (AU): Rieder,S.E.; Emr,S.D.
 TITLE (TI): A novel RING finger protein complex essential for a late step in protein transport to the yeast vacuole
 JOURNAL (SO): Mol. Biol. Cell, 8 (11), 2307-2327 (1997)
 OTHER SOURCE (OS): CA 128:32213
 REFERENCE: 43 (bases 218542 to 219708)
 AUTHOR (AU): Nakamura,T.; Ohmoto,T.; Hirata,D.; Tsuchiya,E.; Miyakawa,T.
 TITLE (TI): Yeast Crv4/Ttp1, a predicted type II membrane protein, is involved in an event important for growth, functionally overlapping with the event regulated by calcineurin- and Mpk1-mediated pathways
 JOURNAL (SO): Mol. Gen. Genet., 256 (5), 481-487 (1997)
 OTHER SOURCE (OS): CA 128:138463
 REFERENCE: 44 (bases 163244 to 165037)
 AUTHOR (AU): Espagne,E.; Balhadere,P.; Begueret,J.; Turcq,B.
 TITLE (TI): Reactivity in vegetative incompatibility of the HET-E protein of the fungus *Podospora anserina* is dependent on GTP-binding activity and a WD40 repeated domain
 JOURNAL (SO): Mol. Gen. Genet., 256 (6), 620-627 (1997)
 OTHER SOURCE (OS): CA 128:214667
 REFERENCE: 45 (bases 98558 to 100377)
 AUTHOR (AU): Mao,C.; Wadleigh,M.; Jenkins,G.M.; Hannun,Y.A.; Obeid,L.M.
 TITLE (TI): Identification and characterization of *Saccharomyces cerevisiae* dihydrosphingosine-1-phosphate phosphatase
 JOURNAL (SO): J. Biol. Chem., 272 (45), 28690-28694 (1997)
 OTHER SOURCE (OS): CA 128:72216
 REFERENCE: 46 (bases 103137 to 103945)
 AUTHOR (AU): Kondoh,O.; Tachibana,Y.; Ohya,Y.; Arisawa,M.; Watanabe,T.
 TITLE (TI): Cloning of the RH01 gene from *Candida albicans* and its regulation of beta-1,3-glucan synthesis
 JOURNAL (SO): J. Bacteriol., 179 (24), 7734-7741 (1997)
 OTHER SOURCE (OS): CA 128:111391
 REFERENCE: 47 (bases 67552 to 68735)
 AUTHOR (AU): Gonzalez,F.J.; Montes,J.; Martin,F.; Lopez,M.C.; Ferminan,E.; Catalan,J.; Galan,M.A.; Dominguez,A.
 TITLE (TI): Molecular cloning of TvDAO1, a gene encoding a D-amino acid oxidase from *Trigonopsis variabilis* and its expression in *Saccharomyces cerevisiae* and *Kluyveromyces lactis*
 JOURNAL (SO): Yeast, 13 (15), 1399-1408 (1997)
 OTHER SOURCE (OS): CA 128:150109

REFERENCE: 48 (bases 41237 to 43709)
 AUTHOR (AU): Motorin,Y.; Le Caer,J.P.; Waller,J.P.
 TITLE (TI): Cysteiny1-tRNA synthetase from *Saccharomyces cerevisiae*. Purification, characterization and assignment to the genomic sequence YNL247w
 JOURNAL (SO): *Biochimie*, 79 (12), 731-740 (1997)
 OTHER SOURCE (OS): CA 129:24853

REFERENCE: 49 (bases 98558 to 100377)
 AUTHOR (AU): Mandala,S.M.; Thornton,R.; Tu,Z.; Kurtz,M.B.; Nickels,J.; Broach,J.; Menzeleev,R.; Spiegel,S.
 TITLE (TI): Sphingoid base 1-phosphate phosphatase: a key regulator of sphingolipid metabolism and stress response
 JOURNAL (SO): *Proc. Natl. Acad. Sci. U.S.A.*, 95 (1), 150-155 (1998)
 OTHER SOURCE (OS): CA 128:151503

REFERENCE: 50 (bases 65395 to 67116)
 AUTHOR (AU): Gaxiola,R.A.; Yuan,D.S.; Klausner,R.D.; Fink,G.R.
 TITLE (TI): The yeast CLC chloride channel functions in cation homeostasis
 JOURNAL (SO): *Proc. Natl. Acad. Sci. U.S.A.*, 95 (7), 4046-4050 (1998)
 OTHER SOURCE (OS): CA 128:319139

REFERENCE: 51 (bases 151141 to 153445)
 AUTHOR (AU): Cazelle,B.; Pokorska,A.; Hull,E.; Green,P.M.; Stanway,G.; Scazzocchio,C.
 TITLE (TI): Sequence, exon-intron organization, transcription and mutational analysis of *prnA*, the gene encoding the transcriptional activator of the *prn* gene cluster in *Aspergillus nidulans*
 JOURNAL (SO): *Mol. Microbiol.*, 28 (2), 355-370 (1998)
 OTHER SOURCE (OS): CA 129:63816

REFERENCE: 52 (bases 48251 to 50618)
 AUTHOR (AU): Lubkowitz,M.A.; Barnes,D.; Breslav,M.; Burchfield,A.; Naider,F.; Becker,J.M.
 TITLE (TI): *Schizosaccharomyces pombe* *isp4* encodes a transporter representing a novel family of oligopeptide transporters
 JOURNAL (SO): *Mol. Microbiol.*, 28 (4), 729-741 (1998)
 OTHER SOURCE (OS): CA 129:119284

REFERENCE: 53 (bases 54264 to 55012)
 AUTHOR (AU): Babst,M.; Wendland,B.; Estepa,E.J.; Emr,S.D.
 TITLE (TI): The Vps4p AAA ATPase regulates membrane association of a Vps protein complex required for normal endosome function
 JOURNAL (SO): *EMBO J.*, 17 (11), 2982-2993 (1998)
 OTHER SOURCE (OS): CA 129:146701

REFERENCE: 54 (bases 149275 to 150765)
 AUTHOR (AU): Silve,S.; Dupuy,P.H.; Ferrara,P.; Loison,G.
 TITLE (TI): Human lamin B receptor exhibits sterol C14-reductase activity in *Saccharomyces cerevisiae*
 JOURNAL (SO): *Biochim. Biophys. Acta*, 1392 (2-3), 233-244 (1998)
 OTHER SOURCE (OS): CA 129:146116

REFERENCE: 55 (bases 27949 to 28578)
 AUTHOR (AU): Caldas,C.; Kim,M.H.; MacGregor,A.; Cain,D.; Aparicio,S.; Wiedemann,L.M.
 TITLE (TI): Isolation and characterization of a pufferfish MLL (mixed lineage leukemia)-like gene (fML1) reveals evolutionary conservation in vertebrate genes related to *Drosophila trithorax*
 JOURNAL (SO): *Oncogene*, 16 (25), 3233-3241 (1998)
 OTHER SOURCE (OS): CA 129:171330

REFERENCE: 56 (bases 218542 to 219708)
 AUTHOR (AU): Rayner,J.C.; Munro,S.
 TITLE (TI): Identification of the MNN2 and MNN5

mannosyltransferases required for forming and extending the mannose branches of the outer chain mannans of *Saccharomyces cerevisiae*
J. Biol. Chem., 273 (41), 26836-26843 (1998)
OTHER SOURCE (OS): CA 130:22764
REFERENCE: 57 (bases 218542 to 219708)
AUTHOR (AU): Lussier, M.; Sdicu, A.M.; Bussey, H.
TITLE (TI): The KTR and MN1L mannosyltransferase families of *Saccharomyces cerevisiae*
JOURNAL (SO): Biochim. Biophys. Acta, 1426 (2), 323-334 (1999)
OTHER SOURCE (OS): CA 130:293055
REFERENCE: 58 (bases 154037 to 156562)
AUTHOR (AU): de Vries, R.P.; Visser, J.; de Graaff, L.H.
TITLE (TI): CreA modulates the XlnR-induced expression on xylose of *Aspergillus niger* genes involved in xylan degradation
JOURNAL (SO): Res. Microbiol., 150 (4), 281-285 (1999)
OTHER SOURCE (OS): CA 131:180701
REFERENCE: 59 (bases 80610 to 81592)
AUTHOR (AU): Ui, S.; Mimura, A.; Ohkuma, M.; Kudo, T.
TITLE (TI): Formation of a chiral acetoinic compound from diacetyl by *Escherichia coli* expressing meso-2,3-butanediol dehydrogenase
JOURNAL (SO): Lett. Appl. Microbiol., 28 (6), 457-460 (1999)
OTHER SOURCE (OS): CA 131:225912
REFERENCE: 60 (bases 211445 to 212528)
AUTHOR (AU): Krappmann, S.; Helmstaedt, K.; Gerstberger, T.; Eckert, S.; Hoffmann, B.; Hoppert, M.; Schnappauf, G.; Braus, G.H.
TITLE (TI): The *aroC* gene of *Aspergillus nidulans* codes for a monofunctional, allosterically regulated chorismate mutase
JOURNAL (SO): J. Biol. Chem., 274 (32), 22275-22282 (1999)
OTHER SOURCE (OS): CA 131:268796
REFERENCE: 61 (bases 137703 to 138530)
AUTHOR (AU): Lombaerts, M.; Peltola, P.H.; Visse, R.; den Dulk, H.; Brouwer, J.
TITLE (TI): Characterization of the *rhp7(+)* and *rhp16(+)* genes in *Schizosaccharomyces pombe*
JOURNAL (SO): Nucleic Acids Res., 27 (17), 3410-3416 (1999)
OTHER SOURCE (OS): CA 132:809
REFERENCE: 62
AUTHOR (AU): Tsai, H.F.; Wheeler, M.H.; Chang, Y.C.; Kwon-Chung, K.J.
TITLE (TI): A developmentally regulated gene cluster involved in conidial pigment biosynthesis in *Aspergillus fumigatus*
JOURNAL (SO): J. Bacteriol., 181 (20), 6469-6477 (1999)
OTHER SOURCE (OS): CA 132:45624
REFERENCE: 63
AUTHOR (AU): DeZwaan, T.M.; Carroll, A.M.; Valent, B.; Sweigard, J.A.
TITLE (TI): *Magnaporthe grisea* *pth1p* is a novel plasma membrane protein that mediates appressorium differentiation in response to inductive substrate cues
JOURNAL (SO): Plant Cell, 11 (10), 2013-2030 (1999)
OTHER SOURCE (OS): CA 132:47358
REFERENCE: 64 (bases 20272 to 22263)
AUTHOR (AU): Layfield, R.; Franklin, K.; Landon, M.; Walker, G.; Wang, P.; Ramage, R.; Brown, A.; Love, S.; Urquhart, K.; Muir, T.; Baker, R.; Mayer, R.J.
TITLE (TI): Chemically synthesized ubiquitin extension proteins detect distinct catalytic capacities of deubiquitinating enzymes
JOURNAL (SO): Anal. Biochem., 274 (1), 40-49 (1999)
OTHER SOURCE (OS): CA 132:20406
REFERENCE: 65 (bases 55690 to 56601)

AUTHOR (AU): Munoz,M.J.; Bejarano,E.R.; Daga,R.R.; Jimenez,J.
 TITLE (TI): The identification of Wos2, a p23 homologue that
 interacts with Wee1 and Cdc2 in the mitotic control of
 fission yeasts
 JOURNAL (SO): Genetics, 153 (4), 1561-1572 (1999)
 OTHER SOURCE (OS): CA 132:177833
 REFERENCE: 66 (bases 149275 to 150765)
 AUTHOR (AU): Zweytick,D.; Hrastnik,C.; Kohlwein,S.D.; Daum,G.
 TITLE (TI): Biochemical characterization and subcellular
 localization of the sterol C-24(28) reductase, erg4p,
 from the yeast *saccharomyces cerevisiae*
 JOURNAL (SO): FEBS Lett., 470 (1), 83-87 (2000)
 OTHER SOURCE (OS): CA 132:331762
 REFERENCE: 67 (bases 51277 to 53277)
 AUTHOR (AU): Cole,C.N.
 TITLE (TI): mRNA export: the long and winding road
 JOURNAL (SO): Nat. Cell Biol., 2 (4), E55-E58 (2000)
 OTHER SOURCE (OS): CA 133:27711
 REFERENCE: 68 (bases 51277 to 53277)
 AUTHOR (AU): Stutz,F.; Bachi,A.; Doerks,T.; Braun,I.C.; Seraphin,B.;
 Wilm,M.; Bork,P.; Izaurralde,E.
 TITLE (TI): REF, an evolutionary conserved family of hnRNP-like
 proteins, interacts with TAP/Mex67p and participates in
 mRNA nuclear export
 JOURNAL (SO): RNA, 6 (4), 638-650 (2000)
 OTHER SOURCE (OS): CA 133:70318
 REFERENCE: 69 (bases 163244 to 165037)
 AUTHOR (AU): Loubradou,G.; Turcq,B.
 TITLE (TI): Vegetative incompatibility in filamentous fungi: a
 roundabout way of understanding the phenomenon
 JOURNAL (SO): Res. Microbiol., 151 (4), 239-245 (2000)
 OTHER SOURCE (OS): CA 133:234784
 REFERENCE: 70 (bases 166037 to 167516)
 AUTHOR (AU): Yu,J.; Woloshuk,C.P.; Bhatnagar,D.; Cleveland,T.E.
 TITLE (TI): Cloning and characterization of avfA and omtB genes
 involved in aflatoxin biosynthesis in three *Aspergillus*
 species
 JOURNAL (SO): Gene, 248 (1-2), 157-167 (2000)
 OTHER SOURCE (OS): CA 133:345391
 REFERENCE: 71 (bases 143978 to 145355)
 AUTHOR (AU): Sanders,P.M.; Lee,P.Y.; Biesgen,C.; Boone,J.D.;
 Beals,T.P.; Weiler,E.W.; Goldberg,R.B.
 TITLE (TI): The arabidopsis DELAYED DEHISCENCE1 gene encodes an
 enzyme in the jasmonic acid synthesis pathway
 JOURNAL (SO): Plant Cell, 12 (7), 1041-1061 (2000)
 OTHER SOURCE (OS): CA 134:25937
 REFERENCE: 72 (bases 145510 to 146577)
 AUTHOR (AU): Cheng,Q.; Thomas,S.M.; Kostichka,K.; Valentine,J.R.;
 Nagarajan,V.
 TITLE (TI): Genetic analysis of a gene cluster for cyclohexanol
 oxidation in *Acinetobacter* sp. Strain SE19 by in vitro
 transposition
 JOURNAL (SO): J. Bacteriol., 182 (17), 4744-4751 (2000)
 OTHER SOURCE (OS): CA 134:37832
 REFERENCE: 73 (bases 163244 to 165037)
 AUTHOR (AU): Saupe,S.J.
 TITLE (TI): Molecular genetics of heterokaryon incompatibility in
 filamentous ascomycetes
 JOURNAL (SO): Microbiol. Mol. Biol. Rev., 64 (3), 489-502 (2000)
 OTHER SOURCE (OS): CA 134:27321
 REFERENCE: 74 (bases 128987 to 130729)
 AUTHOR (AU): Tanaka,A.; Tsuge,T.

TITLE (TI): Structural and functional complexity of the genomic region controlling AK-toxin biosynthesis and pathogenicity in the Japanese pear pathotype of *Alternaria alternata*

JOURNAL (SO): Mol. Plant Microbe Interact., 13 (9), 975-986 (2000)

OTHER SOURCE (OS): CA 134:96037

REFERENCE: 75 (bases 143978 to 145355)

AUTHOR (AU): Stintzi, A.; Browse, J.

TITLE (TI): The Arabidopsis male-sterile mutant, *opr3*, lacks the 12-oxophytodienoic acid reductase required for jasmonate synthesis

JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 97 (19), 10625-10630 (2000)

OTHER SOURCE (OS): CA 133:293530

REFERENCE: 76 (bases 54264 to 55012)

AUTHOR (AU): Amerik, A.Y.; Nowak, J.; Swaminathan, S.; Hochstrasser, M.

TITLE (TI): The Doa4 deubiquitinating enzyme is functionally linked to the vacuolar protein-sorting and endocytic pathways

JOURNAL (SO): Mol. Biol. Cell, 11 (10), 3365-3380 (2000)

OTHER SOURCE (OS): CA 134:82296

REFERENCE: 77 (bases 208451 to 210658)

AUTHOR (AU): Tieu, Q.; Nunnari, J.

TITLE (TI): Mdv1p is a WD repeat protein that interacts with the dynamin-related GTPase, Dnm1p, to trigger mitochondrial division

JOURNAL (SO): J. Cell Biol., 151 (2), 353-366 (2000)

OTHER SOURCE (OS): CA 134:52741

REFERENCE: 78 (bases 208451 to 210658)

AUTHOR (AU): Mozdy, A.D.; McCaffery, J.M.; Shaw, J.M.

TITLE (TI): Dnm1p GTPase-mediated mitochondrial fission is a multi-step process requiring the novel integral membrane component Fis1p

JOURNAL (SO): J. Cell Biol., 151 (2), 367-380 (2000)

OTHER SOURCE (OS): CA 134:52934

REFERENCE: 79 (bases 94126 to 97982)

AUTHOR (AU): Kadoya, T.; Kishida, S.; Fukui, A.; Hinoi, T.; Michiue, T.; Kikuchi, A.

TITLE (TI): Inhibition of Wnt signaling pathway by a novel axin-binding protein

JOURNAL (SO): J. Biol. Chem., 275 (47), 37030-37037 (2000)

OTHER SOURCE (OS): CA 134:233219

REFERENCE: 80 (bases 80610 to 81592)

AUTHOR (AU): Ui, S.; Takusagawa, Y.; Ohtsuki, T.; Mimura, A.; Ohkuma, M.; Kudo, T.

TITLE (TI): Stereochemical applications of the expression of the L-2,3-butanediol dehydrogenase gene in *Escherichia coli*

JOURNAL (SO): Lett. Appl. Microbiol., 32 (2), 93-98 (2001)

OTHER SOURCE (OS): CA 135:353434

REFERENCE: 81 (bases 80610 to 81592)

AUTHOR (AU): Otagiri, M.; Kurisu, G.; Ui, S.; Takusagawa, Y.; Ohkuma, M.; Kudo, T.; Kusunoki, M.

TITLE (TI): Crystal structure of meso-2,3-butanediol dehydrogenase in a complex with NAD⁺ and inhibitor mercaptoethanol at 1.7 Å resolution for understanding of chiral substrate recognition mechanisms

JOURNAL (SO): J. Biochem., 129 (2), 205-208 (2001)

OTHER SOURCE (OS): CA 135:2180

REFERENCE: 82 (bases 41237 to 43709)

AUTHOR (AU): Davidson, E.; Caffarella, J.; Vitseva, O.; Hou, Y.M.; King, M.P.

TITLE (TI): Isolation of two cDNAs encoding functional human cytoplasmic cysteinyl-tRNA synthetase

JOURNAL (SO): Biol. Chem., 382 (3), 399-406 (2001)
 OTHER SOURCE (OS): CA 135:118589
 REFERENCE: 83 (bases 119272 to 121189)
 AUTHOR (AU): Cukovic,D.; Ehltling,J.; VanZiffle,J.A.; Douglas,C.J.
 TITLE (TI): Structure and evolution of 4-coumarate:coenzyme A
 ligase (4CL) gene families
 JOURNAL (SO): Biol. Chem., 382 (4), 645-654 (2001)
 OTHER SOURCE (OS): CA 136:145906
 REFERENCE: 84 (bases 87776 to 89339)
 AUTHOR (AU): Gassama-Diagne,A.; Hullin-Matsuda,F.; Li,R.Y.;
 Nauze,M.; Ragab,A.; Pons,V.; Delagebeaudeuf,C.;
 Simon,M.F.; Fauvel,J.; Chap,H.
 TITLE (TI): Enterophilins, a new family of leucine zipper proteins
 bearing a b30.2 domain and associated with enterocyte
 differentiation
 JOURNAL (SO): J. Biol. Chem., 276 (21), 18352-18360 (2001)
 OTHER SOURCE (OS): CA 136:114413
 REFERENCE: 85 (bases 80610 to 81592)
 AUTHOR (AU): Otagiri,M.; Kurisu,G.; Swaminathan,S.; Ui,S.;
 Yoneda,S.; Ohkuma,M.; Kudo,T.; Kusunoki,M.
 TITLE (TI): Crystallization and preliminary X-ray studies of
 meso-2,3-butanediol dehydrogenase from *Klebsiella*
pneumoniae IAM1063
 JOURNAL (SO): Acta Crystallogr. D Biol. Crystallogr., 57 (PT 6),
 857-859 (2001)
 REFERENCE: 86 (bases 51277 to 53277)
 AUTHOR (AU): Zenklusen,D.; Vinciguerra,P.; Strahm,Y.; Stutz,F.
 TITLE (TI): The yeast hnRNP-Like proteins Yralp and Yra2p
 participate in mRNA export through interaction with
 Mex67p
 JOURNAL (SO): Mol. Cell. Biol., 21 (13), 4219-4232 (2001)
 OTHER SOURCE (OS): CA 135:177841
 REFERENCE: 87 (bases 1 to 226503)
 AUTHOR (AU): Pel,H.J.; de Winde,J.H.; Archer,D.B.; Dyer,P.S.;
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 Stam,H.
 TITLE (TI): Genome sequencing and analysis of the versatile cell
 factory *Aspergillus niger* CBS 513.88
 JOURNAL (SO): Nat. Biotechnol., 25 (2), 221-231 (2007)
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 REFERENCE: 88 (bases 1 to 226503)
 AUTHOR (AU): Pel,H.J.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O.
 Box 1, 2600 MA Delft, THE NETHERLANDS

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AAGGYSGTHTTGAGYGGAGAGAGYGGGAGYGGSG
VNDYTTSSGYGGSSNAGPHGSNMA
NKMDPRVDSMDNRRARHQGMASSSYNAPGQTTAG
PHSSNMANKLDPRVDSLDNRGTL GTQRGF"

exon      complement(6405..6781) /locus-tag="An14g05070"
          /number=1
intron    complement(6782..6839) /locus-tag="An14g05070"
          /number=1
exon      complement(6840..7160) /locus-tag="An14g05070"
          /number=2
intron    complement(7161..7214) /locus-tag="An14g05070"
          /number=2
exon      complement(7215..7365) /locus-tag="An14g05070"
          /number=3
gene      complement(<8900..>1022 /locus-tag="An14g05080"
6)
mRNA      complement(join(<8900.. /locus-tag="An14g05080"
9282,9368..9550,
9634..9898,
10206..>10226))
CDS       complement(join(8900..9 /locus-tag="An14g05080"
282,9368..9550,
9634..9898,
10206..10226))

/inference="profile:COGS:COG0666"
/inference="profile:PFAM:PF00023"
/note="unnamed protein product;
Function: many ankyrin repeat
regions are known to function as
protein-protein interaction
domains. Remark: closest manual
BLASTP homologue:
SWISSPROT:ANK1-HUMAN. Similarity:
ankyrin repeats (ANK) are tandemly
repeated modules of about 33 amino
acids, that occur in a large
number of functionally diverse
proteins mainly from eukaryotes.
Similarity: the predicted ORF
shows similarity also to the ZU5
domain present in ZO-1 and
Unc5-like netrin receptors, which
function remains unknown.
Similarity: the similarity to
ankyrin of H. sapiens and other
proteins is mainly due to the
presence of two ankyrin repeats.
Title: weak similarity to ankyrin
(variant 2.1) -Homo sapiens"
/citation=[5]
/codon-start=1

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/protein-id="CAK42069.1"
/db-xref="GI:134081814"
/translation="MSRATFMIRDCTKNFFQSGK
PTSGNGHTPAIVETLRIELLNGLM
GPASGSLITVISESGEKTMRRVFSGFQPILAVGN
PSLANYLVDELRPSEKTAHRGHE
SIIRILLDFGVKDLNSRDKSGHTPLLHAASMWHT
KIVKLLRTGIPDPNCONAGAHET
IMFGHRWPLPVKLVMKRSLPLETGKMDSSLEDQ
DGFPTLTYATEYGNERIIKLLDA
SDPRAAKTATTELEIFAATRATPELQPVHEGPPV
EATPSELVSRTPKDIVRLWRNN PALNPQH"

exon      complement(8900..9282) /locus-tag="An14g05080"
          /number=1
intron    complement(9283..9367) /locus-tag="An14g05080"
          /number=1
exon      complement(9368..9550) /locus-tag="An14g05080"
          /number=2
intron    complement(9551..9633) /locus-tag="An14g05080"
          /number=2
exon      complement(9634..9898) /locus-tag="An14g05080"
          /number=3
intron    complement(9899..10205) /locus-tag="An14g05080"
          /number=3
exon      complement(10206..10226) /locus-tag="An14g05080"
          /number=4
gene      <11182..>11344 /locus-tag="An14g05090"
mRNA      join(<11182..11234, /locus-tag="An14g05090"
            11281..>11344)
CDS       join(11182..11234, /locus-tag="An14g05090"
            11281..11344)

/note="Similarity: BLASTP
identifies a stretch of similarity
to D. melanogaster genomic
fragment CG6456; there is no
sufficient reason to consider such
a similarity significant."
/codon-start=1
/product="hypothetical protein"
/protein-id="CAK42070.1"
/db-xref="GI:134081815"
/translation="MAGSPNSFPGGNGLSEEF
GWLPGGKPTNCNETIGSR"

exon      11182..11234 /locus-tag="An14g05090"
          /number=1
intron    11235..11280 /locus-tag="An14g05090"
          /number=1
exon      11281..11344 /locus-tag="An14g05090"
          /number=2
gene      <12054..>13438 /locus-tag="An14g05100"
mRNA      join(<12054..12184, /locus-tag="An14g05100"
            12254..12395,
            12454..12995,
            13054..>13438)
CDS       join(12054..12184, /locus-tag="An14g05100"
            12254..12395,
            12454..12995,
            13054..13438)

/inference="profile:COGS:COG3781"
/inference="profile:PFAM:PF05249"
/inference="similar to AA

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exon 12054..12184
 intron 12185..12253
 exon 12254..12395
 intron 12396..12453
 exon 12454..12995
 intron 12996..13053
 exon 13054..13438
 gene <13882..>14418
 mRNA <13882..>14418
 CDS 13882..14418

sequence:PIR:AD2179"
 /note="unnamed protein product;
 Title: strong similarity to
 hypothetical protein alr2987 -
 Nostoc sp"
 /codon-start=1
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 /db-xref="GI:134081816"
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 LNNAAHYRAGTHPHLLTSRSKPRR
 WPLVFRFIKGAIIHAAILLPVFLHAAFTAFVYVLD
 VYVFDTVGLPSSIIIPSLIVVGLM
 LVFRNQTSYNRFWDGRNGMNTIYT CIRNLVRTIV
 TNGYSTAGPPTAAEKEDIERTIRI
 LMSIPFAVKNHLRAEWGAALGNDVAENGVAAF
 NPDYASLLPAGLVGHEDEGLGLPF
 QLTFFVDGFIKRGVERGWFNAPGASQMQAQLNSL
 MDAYGKMETIKLTPIPVAHLIHQK
 QVLALFGCVLPFGMVDDMGWTVPMVSLVIFTLY
 GIEGIGSQLEDFFGYDRNDIKMDA
 IVGDAKTEIDVVLAEWRRMLMASLESATDNGDQHL
 GNGLVVEEVEKPKFMPFDMFLKH RARPSGR"
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 /locus-tag="An14g05100"
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 /number=4
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 /locus-tag="An14g05110"
 /inference="similar to AA
 sequence:UniProtKB:BT004329.1"
 /note="unnamed protein product;
 Similarity: the predicted ORF
 contains an EF-hand,the most
 common domain responsible for
 calcium binding in proteins like
 calmodulin, myosin regulatory
 light chains,parvalbumins,
 troponins C, and neuronal calcium
 sensors. Title: weak similarity to
 hypothetical protein AT4g01140 -
 Arabidopsis thaliana"
 /codon-start=1
 /protein-id="CAK42072.1"
 /db-xref="GI:134081817"
 /translation="MNLPLLLTLTTFLPIATA
 FTSTFENCQNLNRLNQTVHRVHPL
 LEKFSSIHASQSQSSTTTTTLANGTTITVINTT
 SSAIEKIEGVKALLSSQEKIYG
 RLSNCSSDAVSPRNVLKGVKRRDDDDGSCSTLND
 VLDQLVDTLECVLSEATGLLETIL
 DGLFDLLKTIIEGVKLL"

sig-peptide	13882..13941	/locus-tag="An14g05110" /inference="protein motif:SignalP:2.0"
mat-peptide	13942..14415	/locus-tag="An14g05110" /product="unnamed"
exon	13882..14418	/locus-tag="An14g05110" /number=1
gene	complement(<14885..>16307)	/locus-tag="An14g05120"
mRNA	complement(join(<14885..15101,15159..15313,15370..15531,15585..15698,15751..15900,15955..16104,16161..>16307))	/locus-tag="An14g05120"
CDS	complement(join(14885..15101,15159..15313,15370..15531,15585..15698,15751..15900,15955..16104,16161..16307))	/inference="profile:COGS:COG0714" /inference="similar to AA sequence:UniProtKB:NC17E5.27" /note="unnamed protein product; Function: MoxR is a poorly characterized bacterial protein which may be involved in the regulation of formation of active methanol dehydrogenase. Similarity: the predicted ORF shows weak similarity to many putative proteins classified as MoxR-like ATPases. Title: strong similarity to hypothetical conserved protein 17E5.290 - Neurospora crassa" /codon-start=1 /protein-id="CAK42073.1" /db-xref="GI:134081818" /translation="MEDGSEISRLAPELSDLEVA LFLCLAAHQHCRIIDTTDANIHDVA KELALICTNTFGLSYSILDCSSATSLDDFRAELL PPGVYRSSYARPSRSLTTESAGM ISSYHDLRDHKGRLKSAPIEHKQEVNVVIAKFN NHVNDNIQREALELMHKSQLTTPA GVLEAPNNFLFLPLIVRDETHPINPHLNDYLFIS HFHDTEDGYVYLEENNNDWLSDGQL SASSVIHKPEAQMKKGHPYVDSTLLGQLQQLSTT VSMGADIARYQODIVVFLRLSRAV AGGISTRSNLYFKSFSKLLAVLHGIDFLTPSIVA LAARKVFRHRIIVAKPEEDRSLQY GSDLHAVSQVLEYANPDSILDGVLTLLEAPL"
exon	complement(14885..15101)	/locus-tag="An14g05120" /number=1
intron	complement(15102..15158)	/locus-tag="An14g05120"
exon	complement(15159..15313)	/number=1 /locus-tag="An14g05120"

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    )
intron    complement(15314..15369 /number=2
                                         /locus-tag="An14g05120"
    )
exon      complement(15370..15531 /number=2
                                         /locus-tag="An14g05120"
    )
intron    complement(15532..15584 /number=3
                                         /locus-tag="An14g05120"
    )
exon      complement(15585..15698 /number=3
                                         /locus-tag="An14g05120"
    )
intron    complement(15699..15750 /number=4
                                         /locus-tag="An14g05120"
    )
exon      complement(15751..15900 /number=4
                                         /locus-tag="An14g05120"
    )
intron    complement(15901..15954 /number=5
                                         /locus-tag="An14g05120"
    )
exon      complement(15955..16104 /number=5
                                         /locus-tag="An14g05120"
    )
intron    complement(16105..16160 /number=6
                                         /locus-tag="An14g05120"
    )
exon      complement(16161..16307 /number=6
                                         /locus-tag="An14g05120"
    )
gene      <16557..>19301 /number=7
mRNA      join(<16557..16701, /locus-tag="An14g05130"
              16758..16864, /locus-tag="An14g05130"
              16910..17038,
              17088..17676,
              17726..18996,
              19053..>19301)
CDS       join(16557..16701, /locus-tag="An14g05130"
              16758..16864,
              16910..17038,
              17088..17676,
              17726..18996,
              19053..19301)

/inference="profile:PFAM:PF04840"
/inference="profile:PFAM:PF04841"
/note="unnamed protein product;
Complex: VPS16 of S. cerevisiae is
a component of the so called class
C Vps complex, required for
vacuolar protein sorting and
morphology. Function: VPS16 of S.
cerevisiae is required for
vacuolar protein sorting and
vacuolar biogenesis and stability.
Phenotype: S. cerevisiae VPS16
mutants have pleiotropic defects
in vacuolar morphology and
vacuolar protein targeting. Title:
strong similarity to vacuolar
protein sorting-associated protein

```

Vps16 - *Saccharomyces cerevisiae*
vacuole"
/citation=[2]
/citation=[11]
/citation=[13]
/citation=[42]
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/db-xref="GI:134081819"
/translation="MAPSNPLANWERLGDSFYRK
VPIYDAIFDDDDVELENYIIAGAPY
GGAIALHRDESKPYFRDQAQTAKSSIDIYSCSGK
HINRINWEYGTIRGLGWSDKEELL
VITEDGTVRRYFGLHGDFTSFLGNGAEDYGVR
CRFWTSGFVALLSNNQLVAVSNYD
EPRRLLAPCPPEGEVSSWSLIPPAYTLRSRSEVL
LAVDKTVYLVDPTEADKVLQNGP
FKHASVSPITGRFVALITAEGKVWVSSDFQSKYS
EYDPESRVTPRTVDCGDDAVVIA
WEDEVHLIGPNGVAARYYYDGTVHVVPEDGVRL
ITNDTCEFLHKVVDVTEAIFRLGS
TSPASVLLDSIDLEKSKPKADENIQRIRPSLPE
AVDTCVKAAGHEFDITYWQKRLKA
ASFSGSVLDLYNSDEFVEMTEKLRVLKAVRDYQI
GLPLSYEQYMRILTPERLIERLVNR
HEYLLAIRISEYLELPADRIYVHWASQKVKVSTV
DDDVA CKLIVQRLEGKPGISFELI
AQTAYDEGRAHLATQLLNHEPRAGKQVPLLLDME
EDEIALDKAIESGDVVLVNVYLLH
LKTKLPLASFFRTINTRPMASALVETTARGQDTE
LLKDLFYQDDRPIDGSNVLLSEAL
DATDLPRKTEKLQLASRLSDSKDPSVVLQKLL
NEASQLLKVQEA LDKDLADRSEFL
GLSLNETIYRLIRSGYGKRAQKIQSEFRMPEKTF
WWLRRLRALVAKRDWGELEEIGKNK
KSPIGWEPFYNEILGAGNTKLASLFVPKCTNLPA
EDKMEMWVKCGMIAKAGEEAFRAK
NVNALELLQARASGPAAVEIERMINQLRPRK"
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exon 16557..16701
intron 16702..16757
exon 16758..16864
intron 16865..16909
exon 16910..17038
intron 17039..17087
exon 17088..17676
intron 17677..17725
exon 17726..18996
intron 18997..19052
exon 19053..19301
gene complement (<19354..>19996)

mRNA	complement(join(<19354..19554,19615..19907,19981..>19996))	/locus-tag="An14g05140"
CDS	complement(join(19354..19554,19615..19907,19981..19996))	/locus-tag="An14g05140"
		/note="unnamed protein product; Phenotype: ECM1 mutation in <i>S. cerevisiae</i> causes perturbation of the cell surface. Remark: ECM1 of <i>S. cerevisiae</i> is also called YAL059w. Title: similarity to Ecml - <i>Saccharomyces cerevisiae</i> "
		/citation=[39]
		/codon-start=1
		/protein-id="CAK42075.1"
		/db-xref="GI:134081820"
		/translation="MAKSRPQSKHSRAARRAASP SLDVKSLTSLPRAEETTIVQDSI LSERANAGVSKKQSKGAKTRAQRLRQQKVERA EAVMDQLLEKKVTKSEVRAKSVKAR RAEWEDLNRRKTKSMFEALNEEADNMDAMVDVA AASKPAKRSKPAVPTQTPVVEEHE GIDVDDIT"
exon	complement(19354..19554)	/locus-tag="An14g05140"
		/number=1
intron	complement(19555..19614)	/locus-tag="An14g05140"
		/number=1
exon	complement(19615..19907)	/locus-tag="An14g05140"
		/number=2
intron	complement(19908..19980)	/locus-tag="An14g05140"
		/number=2
exon	complement(19981..19996)	/locus-tag="An14g05140"
		/number=3
gene	<20272..>22263	/locus-tag="An14g05150"
mRNA	<20272..>22263	/locus-tag="An14g05150"
CDS	20272..22263	/locus-tag="An14g05150"
		/EC-number="3.1.2.15"
		/inference="profile:COGS:COG5533"
		/inference="profile:COGS:COG5560"
		/inference="profile:PFAM:PF00443"
		/inference="similar to AA sequence:PIR:S67665"
		/note="unnamed protein product; Catalytic activity: ubiquitin C-terminal thiolester + H2O = ubiquitin + thiol. Function: UBP1 of <i>S. cerevisiae</i> has an ATP-independent isopeptidase activity, cleaving at the carboxyl terminus of the ubiquitin moiety in natural or engineered linear fusion proteins, irrespective of their size or the presence of an amino-terminal extension to ubiquitin. Similarity: UBP1 belongs to peptidase family C19;

also known as family 2 of ubiquitin carboxyl-terminal hydrolases. Similarity: although the predicted ORF is shorter than UbP1 of *S. cerevisiae* and the alignment contains several gaps, it shows consistent similarity to several ubiquitin-specific processing proteases. Title: similarity to ubiquitin specific protease UbP1 - *Saccharomyces cerevisiae*"

/citation=[7]
/citation=[12]
/citation=[27]
/citation=[64]
/codon-start=1
/protein-id="CAK42076.1"
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SNYESILQQLQGNPSLVASILVTV
ITLYLAVSYLGPASLSVARIANILVYLTPSRLI
AALDSKTPKSDENPLSLTFFAEKSE
AMQRILGLDDTSFSSLFPRAPAFSSFGTSLSSK
NNVPPGLGNWDNSCYQNSIIQGLA
SLQSLERFLDQNVQLGQKALLSTHQALKDIIER
LNSADSNQRLWTPADLKSMSSWQ
QQDAQEYFSKIVLDQLDEVQQAIRRHTRNLGLKM
AGPQEHVIGSGISQELQESSAGET
RITGNQIFRNPLEGLLAQRVGCICQGWTEGLSLI
PFNCLTVPLGPKFEYDIRECLHHY
MHLEPIEGVECAKCTLLRVQSQLLNLLKQIGDDE
ETPSATPESPKISDALRSSAQERL
QAVEQALEEEDFAEKTL SQKCHIPGKNRVSSSTKS
RQAVVARPPQCLVIHVNRSMF DEN
TGMLRKNYAAVKFPNALDLNFWCLGGVSKNQSEP
SLEAWETNPSVSMLSHAGRGANAG
GHYQLRAVITHYGRHENGHYICRYKPYPTDTFFPAH
VPDAIIEADGDKERDERWYRLSDE
DVQMVSEANVMSQGGAFMLFYAEVEDYSPEAAED
VDSGLAEEEGSAFSSSCTPSETMS
TTSATGDSTSDVSQATSVSTALNVEPRVEKSL
MSDVD"

/locus-tag="An14g05150"
/number=1
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/inference="profile:COGS:COG5126"
/inference="similar to AA
sequence:PIR:I38424"
/note="unnamed protein product;
Function: centrin is a ubiquitous
component of centrosomes and
mitotic spindle poles of diverse
organisms and plays a role in

exon 20272..22263

gene complement(<22652..>23365)

mRNA complement(join(<22652..23018,23085..23287,23363..>23365))

CDS complement(join(22652..23018,23085..23287,23363..23365))

centrosome separation at the time of mitosis. Localization: human centrin is localized at the centrosome of interphase cells and redistributes to the region of the spindle poles during mitosis. Similarity: in the predicted ORF the EF-hands are not well conserved; this fact might have important functional consequences. Similarity: the human centrin sequence has four putative calcium-binding domains as defined by the EF-hand consensus. Title: similarity to centrin - Homo sapiens centrosome"

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SETVEEFADQKEGVIPRGDVRKALVALGLDPTDS
EELHSIIIEAVDPTDTGYVPYEPFL
AVAAAKLRSRSDDMAAEVDAAYRLFTRGSGGVI
TLNHLRRIARELKKEELGDELLKD
MILEANGGAGVHAGVTLEQFHDVMTAGVF"

/locus-tag="An14g05160"

/number=1
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/number=2
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/number=3
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/locus-tag="An14g05170"

/EC-number="1.-.-."
/inference="profile:COGS:COG3118"
/inference="profile:PFAM:PF00085"
/note="unnamed protein product;
Function: thioredoxin participates
in various redox reactions through
the reversible oxidation of its
active center dithiol to a
disulfide, and catalyzes
dithiol-disulfide exchange
reactions. Similarity: the main

exon complement(22652..23018
)
intron complement(23019..23084
)
exon complement(23085..23287
)
intron complement(23288..23362
)
exon complement(23363..23365
)
gene <23835..>25756
mRNA join(<23835..23848,
23890..23947,
24000..24221,
24272..>25756)
CDS join(23835..23848,
23890..23947,
24000..24221,
24272..25756)

exon	23835..23848
intron	23849..23889
exon	23890..23947
intron	23948..23999
exon	24000..24221
intron	24222..24271
exon	24272..25756
gene	<27298..>27621
mRNA	<27298..>27621
CDS	27298..27621

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feature of the predicted ORF,as
well as of the very similar N.
crassa hypothetical protein 17E5.
270, is to contain different
structural domains, including the
thioredoxin and the leucine
zippers in the C-terminal region.
Similarity: the similarity to
chicken thioredoxin and similar
proteins of other species is
limited to a single domain of the
predicted ORF. Title: similarity
to thioredoxin - Gallus gallus"
/citation=[1]
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NGVEYYFGGQGIQTAIPGSTHHGQPMKHLHLGKTE
LPLDVIEEYIQSLAEIYTPESYDL
FLHNCNNFTQDLAMFALGKGIGIPEHIQNLPQIFLS
TPFGQMMKPQIEMALRGVTOGTGA
GTGTGTGTQFTTTSAPTAPAPVTVQGSVRIASN
LAQLEHHLAAAADSCAVIFITSAT
CPFCMKVYPTYDELAEEAGAKATLIKVDISTAMD
VSMKYSVRATPTFTMTFLKGQKLDE
WSGANPAQLRGNVRLLEMAHPHRRHQQLRPLSL
QRPTINYVYKKVPPLDKLVQKLD
PHHEDPRLLSMITYLKHRTSSSTPAADTPLPQDL
PSFATYLTQTCGFLALDHLFALVD
LTRLLFLDPRVSGYFAEPGHTLLTLLSPSAGL
SGCPYNLRIVMLQLCCTLFSTPLY
RDQLTTSSSLLPTLLHLTTSSLLDSHTNLRVVAA
SLAYNLAAALNHNARFAGHADPLSE
ESQVELTASLVEAITQEEESQEALHGLLFLALGLL
VYEASPDASVVDLCKAMGIAETVA
AKRNVKEKVAKEPLIKEVGEELLMKGL"
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/locus-tag="An14g05180"
/locus-tag="An14g05180"
/note="unnamed protein product;
Title: weak similarity to
hypothetical As-rell -Halocynthia
roretzi"
/codon-start=1
/protein-id="CAK42079.1"

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AKLGHQIRGREGATPACQFRPATA
PTNYLSSRLRPLFLRRCTCLCRHIPPVPCIMLIH
GPVLESPSLVMSQTPKHQCCKCVI VAGGP"
exon      27298..27621      /locus-tag="An14g05180"
                               /number=1
gene      complement(<27949..>285 /locus-tag="An14g05190"
78)
mRNA      complement(<27949..>285 /locus-tag="An14g05190"
78)
CDS       complement(27949..28578 /locus-tag="An14g05190"
)

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Title: weak similarity to MLL -
Fugu rubripes"
/citation=[55]
/codon-start=1
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/db-xref="GI:134081825"
/translation="MYPFLPWSQNQSSVRSSLSE
ATTSTQNVSFVSFSGSSCSPTSMF
PPPPPSPTDSLDDITPRKCSFSSGYEMNNSCAFP
SWPNRPSLLSADSDSSTASAYLSD
EDLLFIGSGSPCESAIDEESAAQDTMTGDVDLTT
EQQIQMIRAAAAEEEAQRARFLAQV
QAHAQAQQAMRVAQMAAAERENAKRKRKAIPER
KRRTASASKATVCRA"
exon      complement(27949..28578 /locus-tag="An14g05190"
)
                               /number=1
gene      <28642..>29713      /locus-tag="An14g05200"
mRNA      join(<28642..28681, /locus-tag="An14g05200"
28733..28801,
28901..29001,
29206..29402,
29446..29476,
29582..>29713)
CDS       join(28642..28681, /locus-tag="An14g05200"
28733..28801,
28901..29001,
29206..29402,
29446..29476,
29582..29713)

/note="unnamed protein product;
Title: questionable ORF"
/codon-start=1
/protein-id="CAK42081.1"
/db-xref="GI:134081826"
/translation="MGVNLGVVQSDAGMEVKKID
TVWGGQDPRVEKGGVGGECINRR
ARSIGGVVWTPPLHLPTDKASWRTKKEPKAARIT
WNFPQCWPEKASTGNPACQARRS
GGRGVFVAVRWKMQQSSWMDTREYYHCSSSGSGR
YVDDVGDVAAAFELISPVRCSEL
LKSIIIGPGTKGYLSIIMIYSHRVDSTLI"
exon      28642..28681      /locus-tag="An14g05200"
                               /number=1
intron    28682..28732      /locus-tag="An14g05200"
                               /number=1
exon      28733..28801      /locus-tag="An14g05200"
                               /number=2

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intron	28802..28900	/locus-tag="An14g05200"
exon	28901..29001	/number=2
intron	29002..29205	/locus-tag="An14g05200"
exon	29206..29402	/number=3
intron	29403..29445	/locus-tag="An14g05200"
exon	29446..29476	/number=4
intron	29477..29581	/locus-tag="An14g05200"
exon	29582..29713	/number=5
gene	<30773..>31030	/locus-tag="An14g05210"
mRNA	join(<30773..30823, 30902..>31030)	/locus-tag="An14g05210"
CDS	join(30773..30823, 30902..31030)	/locus-tag="An14g05210"
		/note="unnamed protein product; Title: weak similarity to protein fragment SEQ ID NO:24290 from patent EP1033405-A2 - Arabidopsis thaliana"
		/codon-start=1
		/protein-id="CAK42082.1"
		/db-xref="GI:134081827"
		/translation="MLPMDVDIHPPVCMQMQLVS YQLGPKVTKMVSNAFRLFASRVGF TTHPIPSLESPTPF"
exon	30773..30823	/locus-tag="An14g05210"
intron	30824..30901	/number=1
exon	30902..31030	/locus-tag="An14g05210"
gene	complement(<32776..>347	/number=2
mRNA	complement(join(<32776.. .32888,32979..33084, 33161..33253, 33402..33450, 33632..33776, 33997..34090, 34194..34227, 34305..>34762))	/locus-tag="An14g05220"
CDS	complement(join(32776.. 32888,32979..33084, 33161..33253, 33402..33450, 33632..33776, 33997..34090, 34194..34227, 34305..34762))	/locus-tag="An14g05220"
		/note="unnamed protein product; Title: weak similarity to furin-like protein 1 Furl - Drosophila melanogaster"
		/citation={14}
		/codon-start=1

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/protein-id="CAK42083.1"
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/translation="MRTNNGSGESPLFGSFDSP
CRHSTVDWQVVEGKDTSGREGTVQN
AAHGGVAPRRHHVSWEACLALKSCGWVENAGGYP
GSWDDDGQGSAPISWMDRLDRKC
STQSRGQSGMLGLHTRMRQGEQANVSKSRKSKS
ISKSTGVPQNGNPEYFWKCAEEAE
WNAHDQLKGTQYFLDFHPKRTTAATGAGGSCPA
HESYRIGKRRSPSQKGKLLLIYS
VPKRTIAGAVETIQSSAVRSFIGGGQVQRKPSL
TTEVWAHRQQQQQQPQDEAIQDG
QINSVLVMACDGWCPSLGRSGHGIGVLVMIILNSY
FVWDDQCQFADFHTASCRLRLTS
SRGTYAKKSRIGSFVQIHPNPSSTKYTV"

exon      complement(32776..32888 /locus-tag="An14g05220"
)
intron    complement(32889..32978 /locus-tag="An14g05220"
)
exon      complement(32979..33084 /locus-tag="An14g05220"
)
intron    complement(33085..33160 /locus-tag="An14g05220"
)
exon      complement(33161..33253 /locus-tag="An14g05220"
)
intron    complement(33254..33401 /locus-tag="An14g05220"
)
exon      complement(33402..33450 /locus-tag="An14g05220"
)
intron    complement(33451..33631 /locus-tag="An14g05220"
)
exon      complement(33632..33776 /locus-tag="An14g05220"
)
intron    complement(33777..33996 /locus-tag="An14g05220"
)
exon      complement(33997..34090 /locus-tag="An14g05220"
)
intron    complement(34091..34193 /locus-tag="An14g05220"
)
exon      complement(34194..34227 /locus-tag="An14g05220"
)
intron    complement(34228..34304 /locus-tag="An14g05220"
)
exon      complement(34305..34762 /locus-tag="An14g05220"
)
gene      <35094..>35591 /locus-tag="An14g05230"
mRNA      join(<35094..35340, /locus-tag="An14g05230"

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35443..35474,
35526..>35591)
CDS      join(35094..35340, /locus-tag="An14g05230"
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35526..35591)

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/product="hypothetical protein"
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/translation="MEKAHTTPSGEDRICCTTIS
TGNGSRSTDREIRCTPRSGCSCRRM
PGYGSVCTGFPVWQLELPWSWGIHDPATGLSEQSG
NNFPGVEVCGEGERGQGRQLQKSKGC
IIDMTARSPCAL"

exon      35094..35340 /locus-tag="An14g05230"
          /number=1
intron    35341..35442 /locus-tag="An14g05230"
          /number=1
exon      35443..35474 /locus-tag="An14g05230"
          /number=2
intron    35475..35525 /locus-tag="An14g05230"
          /number=2
exon      35526..35591 /locus-tag="An14g05230"
          /number=3
gene      complement(<35692..>374 /locus-tag="An14g05240"
65)
mRNA      complement(join(<35692. /locus-tag="An14g05240"
.35854,36343..36411,
36584..36607,
36775..36906,
36960..36967,
37367..>37465))

CDS      complement(join(35692.. /locus-tag="An14g05240"
35854,36343..36411,
36584..36607,
36775..36906,
36960..36967,
37367..37465))

/note="unnamed protein product;
Title: questionable ORF"
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/protein-id="CAK42085.1"
/db-xref="GI:134081830"
/translation="MPNHRPARRNKRFLNIYHPP
IQPSIPIIHQDLEVKQTNGLTLYLT
TYWIAIYPSRVMWVDVIVISVMFVDDGDVRLYDK
AIVGYMADGRKHEDYSHSHYILSA
LGGGFATPRTPARVGRLLYEPKRSVAAWNNGAHA
DIERYRKPD SRGQMDMREKDN YGV DNSK"

exon      complement(35692..35854 /locus-tag="An14g05240"
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intron    complement(35855..36342 /locus-tag="An14g05240"
)
          /number=1
exon      complement(36343..36411 /locus-tag="An14g05240"
)
          /number=2
intron    complement(36412..36583 /locus-tag="An14g05240"
)
          /number=2
exon      complement(36584..36607 /locus-tag="An14g05240"

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exon        complement(36775..36906 /number=3
           ) /locus-tag="An14g05240"
intron      complement(36907..36959 /number=4
           ) /locus-tag="An14g05240"
exon        complement(36960..36967 /number=4
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intron      complement(36968..37366 /number=5
           ) /locus-tag="An14g05240"
exon        complement(37367..37465 /number=5
           ) /locus-tag="An14g05240"
gene        <40106..>40899 /number=6
mRNA        join(<40106..40139, /locus-tag="An14g05250"
               40184..>40899) /locus-tag="An14g05250"
CDS         join(40106..40139, /locus-tag="An14g05250"
               40184..40899)
           /EC-number="1.-.-.-"
           /inference="profile:COGS:COG1028"
           /inference="profile:PFAM:PF00106"
           /note="unnamed protein product;
           Function: it is suggested that the
           ORFL15 protein of S. spinosa is
           involved in oxido-reduction during
           spinosyn biosynthesis. Remark:
           Spinosyns are insecticidal
           microicides which are useful for
           the control of arachnids,
           nematodes and insects. Similarity:
           SDR is a very large family of
           enzymes, most of which are known to
           be NAD- or NADP-dependent
           oxidoreductases with different
           specificities. Similarity: the
           predicted ORF shows strong
           similarity to several hypothetical
           and described members of the short
           chain dehydrogenase (SDR) protein
           family. Title: strong similarity
           to protein involved in spinosyn
           biosynthesis ORFL15 from patent
           WO9946387-Al -Saccharopolyspora
           spinosa"
           /codon-start=1
           /protein-id="CAK42086.1"
           /db-xref="GI:134081831"
           /db-xref="GOA:A2R3R8"
           /translation="MAAEQKLVLITGANQGIGFE
           TAKNLILSDNYHVLGSRDPAKGE
           EAAKTLLEAVPGIKGSVSSIQIDVTDQSVDNAAA
           QIKAQYGRILDILVNNAAMSSMKHP
           PSREAMRQILDVNVVVGALSTTEAFDLLRNSSEK
           RLVEVSSSTGSISRADPSSPFHI
           ASATEYRASKAALNMMVLYMCRCLKDEGFKVFGA

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exon	40106..40139	DPGLCATNLTGDPESLRRRNAEAP SDGGERVATVVKGERDADVGVGVGVSFP"
intron	40140..40183	/locus-tag="An14g05250" /number=1
exon	40184..40899	/locus-tag="An14g05250" /number=1
gene	<41237..>43709	/locus-tag="An14g05260"
mRNA	join(<41237..41527, 41586..41762, 41850..43150, 43289..>43709)	/locus-tag="An14g05260"
CDS	join(41237..41527, 41586..41762, 41850..43150, 43289..43709)	/locus-tag="An14g05260"

/EC-number="6.1.1.16"
 /inference="profile:COGS:COG0215"
 /inference="profile:PFAM:PF01406"
 /inference="similar to AA
 sequence:PIR:S63220"
 /note="unnamed protein product;
 Catalytic activity: ATP +
 L-cysteine + tRNA(cys) = AMP +
 pyrophosphate +
 L-cysteinyl-tRNA(cys). Similarity:
 YNL247W of *S. cerevisiae* belongs
 to class-I aminoacyl-tRNA
 synthetase family. Title: strong
 similarity to cysteine--tRNA
 ligase YNL247w - *Saccharomyces
 cerevisiae*"
 /citation=[24]
 /citation=[48]
 /citation=[82]
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 DYFKFDVEFVMNITDVEDDKIILRG
 RQHLFNKYIAEHPVTVPDVLETARKAYSAYIKK
 NLPVDPDTEPENFVAEAQKTVA
 TTSAIAEAAQKLAGIDAASSKAFYDAAQDVFCFY
 LDVTEGSTIPGDAHEIFTKLTKKY
 EDHFMRDMRDLNVLDPAVTRVTEYGGQIADFVE
 KIVANKFGYVTS DGSVYFDIKAFE
 EAGNHYARLEPWNRRNQPLLRDGEGALSRAEKK
 SSDDFALWKASRPGEPSSWSKWCQ
 GRPGWHIECSAMASSCLGSQIDIHSGGIDLAFPH
 HDNELAQSEAYWCEHKQQWVNYFL
 HMGHLSIQGSKMSKSLKNFTTVKDALERGDYTPR
 SLRIVFLLGGWRDGVETIDDLIKN
 ASSWEEKLNFFVKAKDPSSFRSSDEAPTSSET
 LSQALKSTQEKVHEYFCDSFDTPK
 VMAAISLVTTFNALDSQTLDLKVVESMGTVVTQ
 IVTIFGLNGAASSDSCGIGWEGTD
 IPEAAKRFYPLSAMRDTLRQAAILDDTKQASKD
 ILSLCRLRNVDLNFNLGIYLEDRE

		NKPALVRPVTKDMLQAREEQARKALLKQQEKEKQ EKLQERLEKGLNPFVEMFRTSEY SAWDEGIPTKDAAGEPLAKSKSKLRKDWERQK KAHEAWLASQNGK" /locus-tag="An14g05260" /number=1 /locus-tag="An14g05260" /number=1 /locus-tag="An14g05260" /number=2 /locus-tag="An14g05260" /number=2 /locus-tag="An14g05260" /number=3 /locus-tag="An14g05260" /number=3 /locus-tag="An14g05260" /number=4 /locus-tag="An14g05270" /locus-tag="An14g05270"
exon	41237..41527	
intron	41528..41585	
exon	41586..41762	
intron	41763..41849	
exon	41850..43150	
intron	43151..43288	
exon	43289..43709	
gene	<43954..>45254	
mRNA	join(<43954..43984, 44194..44823, 44878..45059, 45108..>45254)	
CDS	join(43954..43984, 44194..44823, 44878..45059, 45108..45254)	/locus-tag="An14g05270" /codon-start=1 /product="hypothetical protein" /protein-id="CAK42088.1" /db-xref="GI:134081833" /translation="MALDNARRVYIQLNNIDLHT ITTDLSRLHVQRLMRLTAKQASDI RELSICSASGGPLSLGYRVLFPSCPLKQASKDLR EALKKLKQCRTLRLISAVEIKHTDY ELAWMGAIIDMTHSVLSAFCETQNSLKSILTLDFRT DNVASLLRGGLERIPSYGPAELSR FPFGSSRLNHLNLANIAGSPGLCERLLHPLY TRYGVNEVSLDLGKAYAENVVLDV LRGMGHRMLEPKLKQYCHSLRVLTMENIIFRYNY WLRFLHSLKREFRRLQEVNLFWEV NTSSESTSLITOWNHTIYDNTQTRVITYTGPPEEH GALTALEKIASEDPLSVHL" /locus-tag="An14g05270" /number=1 /locus-tag="An14g05270" /number=1 /locus-tag="An14g05270" /number=2 /locus-tag="An14g05270" /number=2 /locus-tag="An14g05270" /number=3 /locus-tag="An14g05270" /number=3 /locus-tag="An14g05270" /number=4 /locus-tag="An14g05280" /locus-tag="An14g05280"
exon	43954..43984	
intron	43985..44193	
exon	44194..44823	
intron	44824..44877	
exon	44878..45059	
intron	45060..45107	
exon	45108..45254	
gene	<46541..>47683	
mRNA	join(<46541..47034, 47092..47344, 47501..>47683)	
CDS	join(46541..47034,	/locus-tag="An14g05280"

47092..47344,
47501..47683)

exon 46541..47034
intron 47035..47091
exon 47092..47344
intron 47345..47500
exon 47501..47683
gene <48251..>50618
mRNA join(<48251..48422,
48475..>50618)
CDS join(48251..48422,
48475..50618)

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RDKKMHAFHFHLSQEAQRQLQDK
ILATHAGIEEYSAGYLPWQLLKLKIDASEVNIS
SKDIIKFRPCFFSPLPTDITRTCL
SKQPNKKS PDENSLGYAGRAMP CPSTVALMHYPL
ILDLFREKYATSVRKGFCLDSLTT
LRECGATSKGKWKQPGLELAEKLS TERWQILRI
LEDLEHEVPHAVCDIRQNIQVDRK
KGLTVAEVKAIMRVMVIRIGLDCYRPHFLMPTLM
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/inference="profile:PFAM:PF03169"
/inference="similar to AA
sequence:UniProtKB:SPBC29B5.2"
/note="unnamed protein product;
Function: isp4 of S. pombe is a
membrane oligopeptide transporter.
Remark: isp4 of S. pombe was
originally identified by
subtractive screening as gene
induced during the sexual
differentiation process.
Similarity: the predicted A. niger
protein shows strong similarity to
protein isp4 of S. pombe, which
belongs to the OPT subfamily of
transporters specific for small
oligopeptides (from the C.
albicans OPT1 gene). Title: strong
similarity to protein isp4p
-Schizosaccharomyces pombe plasma
membrane"
/citation={20}
/citation={52}
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DFDYESEHSFPFVRAVVPETDDPGLPVNTFRMW
VLGFIFTIVSGINQFFSLRYPVS"

		HIVSLVAELLAYPCGVFLAKVLPWLTISLGRGGS FTLNPDHRHFNKEHALIVIMSNVS FGYGSADSTNIIQASSARFYNFGLSAGFSVLVVL CAQLLGFGVAGLAAPWLVEPARII WPQVLSNCAMLETLHSRANTVANGWKISRLRFFL YVTAGGEVWYFFPGLMFTALSYFT WICWIAFRNVVVNQLFGMQTGLGLSPITFDWSQV AYNINPLLSPSWAAINVFAGFALF FWIVVPGIYYSNTWFTAYLEPLMTADVDRGTGVY DTARVISADNTLDVDAYRQYSPPY LPATYAFVYGLSFASITAVLTHIGVWHGKEVWAA LKGNKLDIHARLMKSYKKTWPYW YAAIIAIIITAIAIVMEVYHTKLVPYGVFLGLII PAIYMVPCGIIQGITNVNANQLNV LAEFIGGYMEFGKPLANMIFKILSTDVVQGQVYF AMDMKLGHYLIKIPRTLFLMAQGLA TILGALTQAGVTIWMLGHIQDICSSDQSDGFTCP NGRTVYSSSVIWGLVGPRLLYSVG RIYSSLLHFFWIGAIPLITYFLYKYTRKQFWKY INWPLIFVGTYNVPPATGINYSSW ALVNFAFNHFIKKRFFAWWKYNYILAAALDTGL ALSGIVIFFCISYPGAVFPDWGWN TVYVNTADGEGVAYKSMPEVGYFGPANGTWS" /locus-tag="An14g05290" /number=1 /locus-tag="An14g05290" /number=1 /locus-tag="An14g05290" /number=2 /locus-tag="An14g05300" complement(<51277..>532 77) complement(join(<51277.. /locus-tag="An14g05300" .51279,51332..51599, 51656..51726, 51783..51947, 52973..53002, 53059..>53277)) complement(join(51277.. /locus-tag="An14g05300" 51279,51332..51599, 51656..51726, 51783..51947, 52973..53002, 53059..53277)) /inference="profile:COGS:COG0724" /inference="profile:PFAM:PF00076" /inference="similar to AA sequence:SWISSPROT:YRAL.YEAST" /note="unnamed protein product; Complex: YRAL of <i>S. cerevisiae</i> mediates nuclear export of mRNA by interacting with several other protein factors, like Mex67. Function: YRAL of <i>S. cerevisiae</i> is an mRNA-binding protein involved in the nuclear export of mRNA towards the cytoplasm. Remark: although the gene structure looks strange,the strong similarity to known proteins justify the model. Similarity: YRAL <i>S. cerevisiae</i> belongs to the evolutionarily conserved REF (RNA and export
exon	48251..48422	
intron	48423..48474	
exon	48475..50618	
gene	complement(<51277..>532 77)	
mRNA	complement(join(<51277.. /locus-tag="An14g05300" .51279,51332..51599, 51656..51726, 51783..51947, 52973..53002, 53059..>53277))	
CDS	complement(join(51277.. /locus-tag="An14g05300" 51279,51332..51599, 51656..51726, 51783..51947, 52973..53002, 53059..53277))	

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factor binding proteins) family of
hnRNP-like proteins. Title: strong
similarity to RNA annealing
protein Yral - Saccharomyces
cerevisiae nucleus"
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NGTSRGIASIVFSKPDIAAKAKDLNGLLVDGRP
MKIEVVVDASHAPEVSAKPLGER
VAQTKPQPKPATATKAAAGAKGRGRARRPNRG
NRPKPKTVEELDAEMVDYFSTNE
NAGPAEGNAQANGAAPQQAATGGEDLGMAEIS"
exon      complement(51277..51279 /locus-tag="An14g05300"
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intron    complement(51280..51331 /locus-tag="An14g05300"
)
exon      complement(51332..51599 /locus-tag="An14g05300"
)
intron    complement(51600..51655 /locus-tag="An14g05300"
)
exon      complement(51656..51726 /locus-tag="An14g05300"
)
intron    complement(51727..51782 /locus-tag="An14g05300"
)
exon      complement(51783..51947 /locus-tag="An14g05300"
)
intron    complement(51948..52972 /locus-tag="An14g05300"
)
exon      complement(52973..53002 /locus-tag="An14g05300"
)
intron    complement(53003..53058 /locus-tag="An14g05300"
)
exon      complement(53059..53277 /locus-tag="An14g05300"
)
gene      complement(<54264..>550 /locus-tag="An14g05310"
12)
mRNA      complement(join(<54264.. /locus-tag="An14g05310"
.54902,54965..>55012))
CDS       complement(join(54264.. /locus-tag="An14g05310"
54902,54965..55012))
/inference="profile:COGS:COG5491"
/inference="profile:PFAM:PF03357"

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/note="unnamed protein product;
 Function: the *S. cerevisiae*
 homolog Did3p is a class E Vps
 factor, which function in the
 maturation of a late
 endosome/prevacuolar compartment
 into multivesicular bodies that
 then fuse with the vacuole.
 Remark: DID3 of *S. cerevisiae* is
 also called YKL041w. Remark: *S.*
cerevisiae Did3p is probably
 involved in the ubiquitin-mediated
 maturation of multivesicular
 bodies. Title: strong similarity
 to protein involved in vacuolar
 protein sorting Did3 -
Saccharomyces cerevisiae endosome"
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 RIRKQSTIRLHTSRAQLQSVQMQRVN
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 sequence:PIR:T39220"
 /note="unnamed protein product;
 Function: WOS2 of *S. pombe* is a
 cochaperone protein that interacts
 with cdc2 in the control of the
 M-G1 transition. Similarity: WOS2
 of *S. pombe* belongs to the p23 /
 wos2 family. Title: strong
 similarity to cell cycle regulator
 p21 protein wos2p -
Schizosaccharomyces pombe"
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intron	56465..56526	
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		SLLPVNLVNSFDVNAPLTVFAAGDPMYHQYDRAP
		NETYKQALDRTLHDAFNARTRDSEG
		AFWYFNPYPNMGVLEGLYPLGSFISMWKTYFEPT
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		FMTLVLDLERSGKNSAILNETQRD
		DVYTKYWNVANTIINDADEETGCWQVQLHGGEE
		GNYIESSGSAQFVYGLLKGARLGY
		LQKGTPNGVGYTDAADKCYNLVSEFVKEEADGS
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63704..63796))

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/notes="unnamed protein product;
Function: aygl of A. fumigatus has
an unknown function, but it is
contained in the gene cluster
responsible for conidial
pigmentation. Phenotype: aygl null
mutants of A. fumigatus have
yellowish-green conidia. Title:
strong similarity to hypothetical
yellowish-green 1 aygl -
Aspergillus fumigatus"
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64917..>65270)
CDS       join(63948..64102, /locus-tag="An14g05360"
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64917..65270)
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CFDKRGQVFRGRRLPEAYWHKKRN
TKHGDLLYSVEKASRASVQTTTLKRVTVATLSRT
RQVCQYLRFNLAGASCISELGRYL
HVGEAGRLPTSPSPSLEARTGYMLAFYVYAGMIS
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intron	64829..64916	/number=3 /locus-tag="An14g05360"
exon	64917..65270	/number=3 /locus-tag="An14g05360"
gene	<65395..>67116	/number=4 /locus-tag="An14g05370"
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 the conidial pigmentation gene
 cluster; abrl mutants have brown
 conidia, and the proposed function
 of abrl is multicopper oxidase.
 Title: strong similarity to cell
 surface ferroxidase precursor Fet3
 - Saccharomyces cerevisiae plasma
 membrane"
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 YHVQIPVLLDEFIVPSDHPYGGQELPDAVLFN
 DMHNTKISVKPGTTYLIHVVCMGN
 FPGHALVIDDHDMTIVGMDGIAVEPHFLPPQYLR
 VAVGQRVDILLTKNDTSKNYAIW
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exon	66909..67116	/locus-tag="An14g05370" /number=3
gene	complement(<67552..>68735)	/locus-tag="An14g05380"
mRNA	complement(join(<67552.. .67985,68039..>68735))	/locus-tag="An14g05380"
CDS	complement(join(67552.. 67985,68039..68735))	/locus-tag="An14g05380" /EC-number="1.4.3.3" /inference="profile:COGS:COG0665" /inference="profile:PFAM:PF01266" /note="unnamed protein product; Catalytic activity: the D-amino acid oxidase catalyzes the reaction: D-Amino acid + H2O + O2 = 2-Oxo acid + NH3 + H2O2. Catalytic activity: the D-amino acid oxidase has a wide specificity for D-amino acids, acting also on glycine. Cofactor: D-amino acid oxidase is a flavoprotein (FAD is the cofactor). Title: strong similarity to D-amino acid oxidase DAO1 - Trigonopsis variabilis" /citation=[47] /codon-start=1 /protein-id="CAK42099.1" /db-xref="GI:134081844" /db-xref="GOA:A2R3T1" /translation="MAEKETIVVIGYVVSQCHPL NHNNSTTNHPHFQPNRAGIIGLT TALYIQORLSPSQRVLIAARDFPHSTSLNYPASPW AGAHYRPVPGSNAQHTREETQARR TYAHFKTLAAQEPGAGVQSTTGIEYLENPPAEYL NEKNIQAAYGHLDGFEYLQPGQMP GDVKWAVKYKTFVNVSPVYCAWLLREFVLRGGEV KEYTFVDLREGFYLAERVRAVNC SGLFGFDEKSYIIRGQTCLVRNPCSATITRQNSD GSWSFCIPRPLGGGTIIIGGKQPH NWDPNPMSMETRAQLLANAAKWPFFEEGSKEEFDV IRDIVGRRPAREGGMRIEVEKINQ QGEVIVHAYGAGGRGFELSWGVAEDVYDLMRQNG LIKAKASL"
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gene	<73435..>78401	
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/note="unnamed protein product;
 Title: weak similarity to
 hypothetical Ena-VASP-like protein

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QNTAWKKNFSSSEAGLRRLVLLLEGIQKWARANP
DTWRKEAIRAGLKTALFAFVGLML
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NGDFWDDASPVAAEYRGKQDSMSGESAWERIRRQ
NNVSAQRETRSTVSRPAPSSTASA
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92)       /locus-tag="An14g05430"
mRNA      complement(join(<80610.
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81545..81592))
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          /note="unnamed protein product;
Similarity: SDR is a very large
family of enzymes,most of which
are known to be NAD- or
NADP-dependent oxidoreductases
with different specificities.
Similarity: the predicted ORF
shows strong similarity to several
hypothetical and described members
of the short chain dehydrogenase
(SDR) protein family. Title:
similarity to meso-2,3-butanediol
dehydrogenase (D-acetoin forming)
budC - Klebsiella pneumoniae"
          /citation=[59]
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		TETEFSSGFEGQKGAFNFAQNVLPPLPAESQGG LKYPPTLIFTGATASVKGSAQFAS FAAGKFALRALAQSLAREFGPGKIHVSHVIDGV IDIPRTKGWVFEKEDAKLDPEAIA DSYWHLHTQPRTTFGFELDLRPYVERW"
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gene	<83874..>84647	/locus-tag="An14g05450"
mRNA	<83874..>84647	/locus-tag="An14g05450"
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gene	<85682..>87100	
mRNA	join(<85682..85731, 85821..86058, 86116..86309, 86392..>87100)	
CDS	join(85682..85731, 85821..86058, 86116..86309, 86392..87100)	/locus-tag="An14g05460"
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exon        86392..87100      /locus-tag="An14g05460"
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CDS          complement(join(87776.. /locus-tag="An14g05470"
        88536,88589..89339))

        /note="unnamed protein product;
        Function: enterophilins are a new
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        function associated with
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        VDQLKSGISQLKSSIGQSGNETVFLRSVDVRLSK
        NVEQIQSDVEHLQTDVCGCRVEIS
        KLHATISQLRTDLITLQHETSRLTSVFNRFSLI
        EARNMKHSERVRFNLAHTTHAPIT
        PVPVVEEDGSLQWPEYFPRTVWRFWCLKKRSRIN
        RLALQLAEFYQLGGYEWGRMHQEQ
        TLFASDSDSDDYPNLSRAEAVRLYPEAAHQ
        ALAATLGLVYYKIRNEVGEGPNAS
        ITRPPKRQEEAISATSSKEKPKVMARRPTVSPT
        TLKRLITGPSVESKSLTSEESDKL
        GWNAYSDVSDDTMSKLRGIVSDEVGTLRLALEKG
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        KAGSRNSKAAPDEPTLPNTIPTEVLSISSDHAE
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gene        <91050..>91256      /locus-tag="An14g05480"
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sig-peptide 91050..91127

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gene	<92137..>93393	/locus-tag="An14g05490"
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CDS	92137..93393	/locus-tag="An14g05490"
sig-peptide	92137..92205	/inference="profile:COGS:COG5160" /inference="profile:PFAM:PF02902" /inference="similar to AA sequence:UniProtKB:AF260129.1" /note="unnamed protein product; Similarity: the BLASTP alignment is very nice, but limited to the C-terminal part of the predicted ORF. Title: similarity to axin-associating molecule Axam - Rattus norvegicus" /citation=[79] /codon-start=1 /protein-id="CAK42111.1" /db-xref="GI:134081856"
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gene	complement(<94126..>97982)	/locus-tag="An14g05500"
mRNA	complement(join(<94126..94820,94895..>97982))	/locus-tag="An14g05500"
CDS	complement(join(94126..94820,94895..97982))	/locus-tag="An14g05500"

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LFLFLFFFFFHHFFSFFSPITHLPI
FRVRYLESEYNSFFFLAIELVLPLSLSPKELV
SRLLLTMSGVFTSMRPSVEDHPM
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RKQKHTIAGREANERNSAARAL
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MRSSYELDRAQDNLMLNLAQVRSRFT
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GNDRSTRRATPRRVFREPVVET
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VDWPSQTFEFLGRAVSAVSLFYPEKPIEGR
TESVYADRWRQIQEERQKALPSH
GRVSGQKTVATLLSGDFLTKRSALTCTYTRGEWLN
DEVINGYALIVLTLRRKNHNAGR
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100034..100377))

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/inference="similar to AA
sequence:PIR:S38127"
/note="unnamed protein product;
Function: YSR3 of *S. cerevisiae* is
involved in regulating ceramide
and phosphorylated sphingoid base
levels, and modulates stress
responses through sphingolipid
metabolites. Remark: YSR3 of *S.*
cerevisiae is also called YKR053c.
Similarity: *A. niger* EST
EMBLEST:BE760128 comprises part of
the putative 5'-UTR of the gene
and part of exon 1. Title: strong
similarity to
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phosphatase Ysr3 -*Saccharomyces*
cerevisiae"
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ILFWCGYTSLGRGMVHLLASGVFFSGFIKDLLCL
PRPLSPPLQRITMSGSALEYGFP
STHSTNAVSVAAAYALALNLSSESTLSPQVNIALQ
AITLYVCSIVLGRLYCGMHGFFD
VVIGCLLGFLLAFLQYTLGPTIDEYVLSATGRGA
TLVILLILGLVRIHPEPADDCPCF
DDSVAFAGVMLGAQVAYWHIARLSLVWDEVPAT
VPFEFRQVGLVKTSRLRVIGVLMML
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RNASQYTKVPSQLRDHEVLPGFSE
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mRNA	complement(join(<101552..101717, 101818..101872, 102049..102103, 102196..>102291))	/locus-tag="An14g05520"
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mRNA	join(<103137..103259, 103323..103526, 103586..>103945)	/locus-tag="An14g05530"
CDS	join(103137..103259, 103323..103526, 103586..103945)	/locus-tag="An14g05530"
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functions is the regulation of
beta-1,3-glucan synthase, which
synthesizes the main component of
the fungal cell wall. Similarity:
belongs to the ras transforming
proteins. Title: strong similarity
to GTP-binding protein rho1 from
patent WO9738129-A1 - Candida sp"
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                                     Title: similarity to essential
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83)
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Remark: this ORF is a putative
alginate lyase by homology.
Similarity: belongs to the
NADPH:quinone reductase and
related Zn-dependent
oxidoreductases. Similarity: the
ORF shows similarity to several
oxidoreductases with different
specificities. Title: strong
similarity to protein from patent
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MATQIARVVDLDPVVITTSRPTIQFTKDMGAT
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mRNA      complement(join(<107589 /locus-tag="An14g05560"
..107677,
107764..107819,
107918..107986,
108097..108183,
108460..108535,
108574..>108580))
CDS       complement(join(107589. /locus-tag="An14g05560"
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107918..107986,
108097..108183,
108460..108535,
108574..108580))
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CLVDSLNSVLDVGVADPSIGKE
WGDGGVMEIPEHCGDALETRLIRRNECLCHCSLS
STVTILIPWREAQVSDVLRAGVNL
HVEAFVSMQLIKDLMAESSVIPRGS"
sig-peptide complement(join(108468. /locus-tag="An14g05560"
.108535,
108574..108580))
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motif:SignalP:2.0"
mat-peptide complement(join(107592. /locus-tag="An14g05560"
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108097..108183,
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intron    complement(107678..1077 /locus-tag="An14g05560"
63)
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exon      complement(107764..1078 /locus-tag="An14g05560"
19)
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intron    complement(107820..1079 /locus-tag="An14g05560"
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exon      complement(107918..1079 /locus-tag="An14g05560"
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exon      complement(108460..108535) /number=4 /locus-tag="An14g05560"
intron    complement(108536..108573) /number=5 /locus-tag="An14g05560"
exon      complement(108574..108580) /number=5 /locus-tag="An14g05560"
gene      complement(<109706..>11182) /number=6 /locus-tag="An14g05570"
mRNA      complement(join(<109706..110389,110813..110968,111117..>111182)) /locus-tag="An14g05570"
CDS       complement(join(109706..110389,110813..110968,111117..111182)) /locus-tag="An14g05570"

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Aspergillus niger"
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SRLEPLCSSPTPCPLSVRTEDISASGYPDLLRFTV
DSAPSYSLNFHHEPTSPTRLGLLF
PPPTISRTKFPDPPDRRRSKGNKKKTLKPHSS
QKEKRIDNHHKLPSTKSLINRKM
DMSSKFIEILDPNDRPRMSDCDVRLEDVLADHE
ALVTRPRSSTQSSSKPSLDNRLDR
DAPTSPTRWRKRLSTILVPARRGST"

sig-peptide complement(111120..111182) /locus-tag="An14g05570"
mat-peptide complement(join(109709..110389,110813..110968,111117..111119)) /inference="protein motif:SignalP:2.0" /locus-tag="An14g05570"
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intron    complement(110390..110812) /number=1 /locus-tag="An14g05570"
exon      complement(110813..110968) /number=1 /locus-tag="An14g05570"
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 112218..>112508)
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 112218..112508)
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 MAVGGSHTWTYDQGTWKETKEEPLDWRIDYQTNK
 RRARKAPTGGSGAPVGTGYHLLVIG
 HQHVKKIDANTYETHLTGSKYKLAYSASSNAWS
 IPTVKKQREREVELLDDAKQRVQG
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 intron 112172..112217 /locus-tag="An14g05580"
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 exon 112218..112508 /locus-tag="An14g05580"
 /number=2
 gene <113124..>114242 /locus-tag="An14g05590"
 mRNA join(<113124..113934, /locus-tag="An14g05590"
 113983..>114242)
 CDS join(113124..113934, /locus-tag="An14g05590"
 113983..114242)
 /inference="profile:COGS:COG3145"
 /inference="profile:PFAM:PF03171"
 /note="unnamed protein product;
 Remark: similarity to human
 sequence 203 from patent
 W00129221-A/203. Remark: this ORF
 represents a putative DNA repair
 protein. Title: similarity to
 sequence 203 from patent
 W00129221-A - Homo sapiens"
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 RNELPFYRVRYTIRRGGTETSTINTPRYTIVFGVD
 DSTSFVIENSESTSSNSETSVQDD
 TTNLLDPPPANSPILVDSKTRTPTLESKSKSKY
 RCRPRPIPPCLDILRQAVEKATDD
 GTRYNFVLVNYATGDDSIYHSDDERFLGQNPT
 IASLSLGAGRDFFLLKHKPAKPLK
 FPLKSGDMLIMRGETQSNWLHVPKRKGLQGSAG
 ALGRINITFRAVVPGGTENNYYRY
 NVGDGEVYRWRDEEGKMVATTE"
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 intron 113935..113982 /locus-tag="An14g05590"

exon	113983..114242	/number=1 /locus-tag="An14g05590"
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mRNA	complement (join (<114314..114481, 114528..>115364))	/locus-tag="An14g05600"
CDS	complement (join (114314..114481, 114528..115364))	/locus-tag="An14g05600"
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exon	complement (114314..114481)	/locus-tag="An14g05600"
intron	complement (114482..114527)	/number=1 /locus-tag="An14g05600"
exon	complement (114528..115364)	/number=1 /locus-tag="An14g05600"
gene	complement (<115782..>117895)	/number=2 /locus-tag="An14g05610"
mRNA	complement (join (<115782..115925, 116023..116208, 116389..116437, 116929..117066, 117455..117654, 117890..>117895))	/locus-tag="An14g05610"
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VPDILSIISLAPRMGCTPESMDPVTGVCCLVEAAL
RTTRHCQTAVARPLKYDIPLSLSR
FKLAWLFTGRPLCDYGILIDEESMLFISDITSV
SDTGRNDYAFYFMIHHPLCQFATG
HATFKGPVSETFVVQLLTMR"
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          /number=1
exon      complement(116023..116208) /locus-tag="An14g05610"
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intron    complement(116209..116388) /locus-tag="An14g05610"
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exon      complement(116389..116437) /locus-tag="An14g05610"
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intron    complement(116438..116928) /locus-tag="An14g05610"
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exon      complement(116929..117066) /locus-tag="An14g05610"
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intron    complement(117067..117454) /locus-tag="An14g05610"
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exon      complement(117455..117654) /locus-tag="An14g05610"
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intron    complement(117655..117889) /locus-tag="An14g05610"
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exon      complement(117890..117955) /locus-tag="An14g05610"
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gene      <117920..>118997 /locus-tag="An14g05620"
mRNA      join(<117920..118177, /locus-tag="An14g05620"
            118295..118597,
            118734..>118997)
CDS       join(117920..118177, /locus-tag="An14g05620"
            118295..118597,
            118734..118997)

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Aspergillus niger"
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GNTVSRNLDRGILYQPSLATPRHEIIGSLRPLD
DEESIAPSWSWVSNPNPVKGGGET

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exon          118295..118597      /locus-tag="An14g05620"
intron        118598..118733      /number=2
exon          118734..118997      /locus-tag="An14g05620"
gene          complement(<119272..>12 /number=3
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mRNA          complement(join(<119272 /locus-tag="An14g05630"
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120879..121016,
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CDS           complement(join(119272. /locus-tag="An14g05630"
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120386..120822,
120879..121016,
121097..121189))

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/note="unnamed protein product;
Catalytic activity: ATP +
4-coumarate + CoA = AMP +
pyrophosphate + 4-coumaroyl-CoA.
Pathway: flavonoids, stilbene and
lignin biosynthesis. Remark: the
phenylpropanoid enzyme
4-coumarate:coenzyme A ligase
(4CL) plays a key role in general
phenylpropanoid metabolism. 4CL is
related to a larger class of
prokaryotic and eukaryotic
adenylate-forming enzymes and
shares several conserved peptide
motifs with these enzymes.
Similarity: belongs to the
Acyl-CoA synthetases
(AMP-forming)/AMP-acid ligases II.
Title: strong similarity to
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Populus balsamifera"
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 RPWRVVIAPVPLFAAAAAPSSHFGSLKAGHINYVM
 RRFDLPLFLQTVEKYQVTEMAIVP
 PIATAIIMHPMSYERGYLRSIRASNLGAAPMDKD
 AQKRFORLLGPGANCTQVVGMTET
 CCIATMRNDEGDETGSGVGRLVFNMEAKLVDDNG
 TDISDYGVRGELCVRGPAVTPGYF
 NNPVANAESFDEQGFHTGDIAYCDCATQKWYIV
 DRKKELIKVRGFQVAPPELEAVLL
 AHPLIVDAAVIGLRDVPVPGTELPVVRPETD
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exon	complement(119883..120299)	/locus-tag="An14g05630"
intron	complement(120300..120385)	/locus-tag="An14g05630"
exon	complement(120386..120822)	/locus-tag="An14g05630"
intron	complement(120823..120878)	/locus-tag="An14g05630"
exon	complement(120879..121016)	/locus-tag="An14g05630"
intron	complement(121017..121096)	/locus-tag="An14g05630"
exon	complement(121097..121189)	/locus-tag="An14g05630"
gene	complement(<121271..>122416)	/locus-tag="An14g05640"
mRNA	complement(join(<121271..121409, 121457..121657, 121705..121797, 121861..122051, 122150..122275, 122396..>122416))	/locus-tag="An14g05640"
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TQTATPRPQLPNAARVWGGLPAGG
GLSARLAAIGLSDPFPTTRNTKTRAPPARPVHAN
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exon	complement(121861..122051)	/locus-tag="An14g05640"
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intron	complement(122052..122149)	/locus-tag="An14g05640"
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		/number=5
intron	complement(122276..122395)	/locus-tag="An14g05640"
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gene	<122711..>127337	/locus-tag="An14g05650"
mRNA	join(<122711..122827, 122948..123005, 123087..123243, 123306..123409, 123871..124023, 124127..124263, 124490..124605, 124682..124801, 124889..124955, 125041..125228, 125358..125490, 125911..126029, 126093..126179, 126273..126578, 126625..126770, 126836..127004, 127202..>127337)	/locus-tag="An14g05650"
CDS	join(122711..122827, 122948..123005, 123087..123243,	/locus-tag="An14g05650"

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LKCSTGQQNAKSLRLGLALYMLGV
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 exon 122948..123005
 intron 123006..123086
 exon 123087..123243
 intron 123244..123305
 exon 123306..123409
 intron 123410..123870
 exon 123871..124023

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intron	124264..124489	/number=6 /locus-tag="An14g05650"
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exon	124889..124955	/number=8 /locus-tag="An14g05650"
intron	124956..125040	/number=9 /locus-tag="An14g05650"
exon	125041..125228	/number=9 /locus-tag="An14g05650"
intron	125229..125357	/number=10 /locus-tag="An14g05650"
exon	125358..125490	/number=10 /locus-tag="An14g05650"
intron	125491..125910	/number=11 /locus-tag="An14g05650"
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intron	126030..126092	/number=12 /locus-tag="An14g05650"
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exon	126273..126578	/number=13 /locus-tag="An14g05650"
intron	126579..126624	/number=14 /locus-tag="An14g05650"
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intron	126771..126835	/number=15 /locus-tag="An14g05650"
exon	126836..127004	/number=15 /locus-tag="An14g05650"
intron	127005..127201	/number=16 /locus-tag="An14g05650"
exon	127202..127337	/number=16 /locus-tag="An14g05650"
gene	<127622..>128417	/number=17 /locus-tag="An14g05660"
mRNA	join(<127622..127779, 128125..128227, 128313..>128417)	/locus-tag="An14g05660"
CDS	join(127622..127779, 128125..128227, 128313..128417)	/locus-tag="An14g05660"

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 /db-xref="GI:134081872"
 /translation="MPRELGCGEVYGMGMPTVR

exon	127622..127779	QPDGIRVGALSPLISGMAIRVGGR GIMPTGKRTRDAGQLQIKPCRSSYSPPFVEQLSQQ ELELPSLGRAERGIFTPLESGQMY QNKRIILPFASSRVDRAA" /locus-tag="An14g05660" /number=1
intron	127780..128124	/locus-tag="An14g05660" /number=1
exon	128125..128227	/locus-tag="An14g05660" /number=2
intron	128228..128312	/locus-tag="An14g05660" /number=2
exon	128313..128417	/locus-tag="An14g05660" /number=3
gene	<128987..>130729	/locus-tag="An14g05670"
mRNA	join(<128987..130216, 130286..>130729)	/locus-tag="An14g05670"
CDS	join(128987..130216, 130286..130729)	/locus-tag="An14g05670" /inference="profile:PFAM:PF00172" /inference="similar to AA sequence:UniProtKB:AB035491.1" /note="unnamed protein product; Remark: the Japanese pear pathotype of <i>Alternaria alternata</i> produces host-specific AK-toxin and causes black spot of Japanese pear. Transformation of the wild type with AKTR-1- and AKT3-1-targeting vectors produced toxin-deficient (Tox-), nonpathogenic mutants. Title: similarity to AK-toxin regulating protein AktR-1 - <i>Alternaria</i> <i>alternata</i> " /citation={ 74} /codon-start=1 /protein-id="CAK42128.1" /db-xref="GI:134081873" /translation="MHTCVVVKIIIVDLRDRHRRR CIKNIGQERQSKRKSCDACAQKKL RCSMTFPSCSRCIQSRREPCVYPQSSIPVQAPNLD DAQDNIVTSSGSLHSVSVCAGIIP GGTTWALPTYFDTPTSTADEVNDVSGSSWSPETP TNAELAFQTVNESTMFPMQDVSLM NSPPWQEDLHERPETLGLIEFFSGSLDSCSPAMY IPPTMGSSPVTMVPPTPATLPGDS YATGGGLSMSSVSPGYFDNFWDNMASTDEDHET WRFGTYYTDSRSGSGFGQNFLPKTS HHSPGDIGDLYQELFSLREYPGLALQRQFYSPF LHHELQGYAMQSLGQPISTTLSSI SSYASYLEACDTFDLSMHDGERLAAEGCVVALH AVCVQQILSIFGDNFATTGFSKLP NFAGDQGHETETPVDILLRMTQRVYKLHEDVLRTP HEDETDWRRWKFAESLRNIFAN IIRTLAGRARRYNGINIDPLDSAILLLQLPLPAPE EMWRARSEGEWMIARAQTORQSWAR GVDGSMPLPALRTLQQLLVLEEVS SVSTLLLPIT RMLILCAKLNAGASYG" /locus-tag="An14g05670" /number=1
exon	128987..130216	/locus-tag="An14g05670"
intron	130217..130285	/locus-tag="An14g05670"

exon	130286..130729	/number=1 /locus-tag="An14g05670" /number=2
gene	<131085..>131662	/locus-tag="An14g05680"
mRNA	join(<131085..131323, 131388..131502, 131555..131602, 131645..>131662)	/locus-tag="An14g05680"
CDS	join(131085..131323, 131388..131502, 131555..131602, 131645..131662)	/locus-tag="An14g05680" /codon-start=1 /product="hypothetical protein" /protein-id="CAK42129.1" /db-xref="GI:134081874" /translation="MHGSKRDRLLSAKQKLLGAC MSENWTWGAWLAETPKSGHTAMP RPLTTNMQAVRQAGRQADRLEDEESRPDGEQGP GSLLAFFPMVTSGGGPASTRGIYL GGFFVPLVLSIAAISSEDELVNISWVVDWSRRVPL FSY"
exon	131085..131323	/locus-tag="An14g05680" /number=1
intron	131324..131387	/locus-tag="An14g05680" /number=1
exon	131388..131502	/locus-tag="An14g05680" /number=2
intron	131503..131554	/locus-tag="An14g05680" /number=2
exon	131555..131602	/locus-tag="An14g05680" /number=3
intron	131603..131644	/locus-tag="An14g05680" /number=3
exon	131645..131662	/locus-tag="An14g05680" /number=4
gene	<134201..>135346	/locus-tag="An14g05690"
mRNA	join(<134201..134238, 134452..134502, 134768..134993, 135113..>135346)	/locus-tag="An14g05690"
CDS	join(134201..134238, 134452..134502, 134768..134993, 135113..135346)	/locus-tag="An14g05690" /note="unnamed protein product; Title: questionable ORF" /codon-start=1 /protein-id="CAK42130.1" /db-xref="GI:134081875" /translation="MDMNPVGSNFSRGSSGDIPR LGYRVGAFKRRLYLPGVVKSIIHPPI YYEDLPNVADDYLEGASFPHHKPSHVCPESFYNL FVQYKLDEITGRKEGWRPMDRDNQ IRADGSATCYECVRDNRGYDSLGSLSLMEK RIVDPFDRNTPRGVEIIIEGKAML FIGTFISLFHILITLYDSTFAS"
exon	134201..134238	/locus-tag="An14g05690" /number=1
intron	134239..134451	/locus-tag="An14g05690" /number=1
exon	134452..134502	/locus-tag="An14g05690"

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intron      134503..134767      /number=2
                                         /locus-tag="An14g05690"
exon        134768..134993      /number=2
                                         /locus-tag="An14g05690"
intron      134994..135112      /number=3
                                         /locus-tag="An14g05690"
exon        135113..135346      /number=3
                                         /locus-tag="An14g05690"
gene        complement(<135466..>13 /number=4
                                         /locus-tag="An14g05700"
6476)
mRNA        complement(join(<135466 /locus-tag="An14g05700"
..135580,
135676..135753,
136059..136189,
136290..136364,
136405..>136476))
CDS         complement(join(135466. /locus-tag="An14g05700"
.135580,135676..135753,
136059..136189,
136290..136364,
136405..136476))

                                         /note="unnamed protein product;
                                         Title: strong similarity to
                                         hypothetical protein encoded by
                                         An01g10130 - Aspergillus niger"
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                                         /db-xref="GI:134081876"
                                         /translation="MPMKDSRQLTCRLNSWIRLQ
                                         LEYRAGIIYSDTLTRKKPIVPSGT
                                         KPRCNRYLVQHYLYGIKRSCPARNSGSKCSGCTD
                                         AHDFMDARMENAKELQKVLDSFPS
                                         RIEGSWIIIPDIHTSAMSATEDDSGVMITGLGVLSG
                                         CTLAAFKDRANWNDDDGIPG"
exon        complement(135466..1355 /locus-tag="An14g05700"
80)
                                         /number=1
intron      complement(135581..1356 /locus-tag="An14g05700"
75)
                                         /number=1
exon        complement(135676..1357 /locus-tag="An14g05700"
53)
                                         /number=2
intron      complement(135754..1360 /locus-tag="An14g05700"
58)
                                         /number=2
exon        complement(136059..1361 /locus-tag="An14g05700"
89)
                                         /number=3
intron      complement(136190..1362 /locus-tag="An14g05700"
89)
                                         /number=3
exon        complement(136290..1363 /locus-tag="An14g05700"
64)
                                         /number=4
intron      complement(136365..1364 /locus-tag="An14g05700"
04)
                                         /number=4
exon        complement(136405..1364 /locus-tag="An14g05700"
76)
                                         /number=5

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gene      complement(<137703..>13 /locus-tag="An14g05710"
8530)
mRNA      complement(join(<137703 /locus-tag="An14g05710"
..137767,
137825..137999,
138078..138298,
138437..>138530))
CDS       complement(join(137703. /locus-tag="An14g05710"
.137767,137825..137999,
138078..138298,
138437..138530))

/inference="profile:COGS:COG0553"
/note="unnamed protein product;
Similarity: although the
similarity to Rhp16 of S. pombe is
weak, some motifs in the predicted
ORF suggest that it might be
involved in DNA binding and
repair. Title: weak similarity to
RAD16 nucleotide excision repair
protein homolog rhp16p -
Schizosaccharomyces pombe"
/citation={32}
/citation={61}
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/protein-id="CAK42132.1"
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/translation="MARYDFYMSAMFLGSWHTG
SWPRQCEHLGAAGKIKRKRAGPCN
IRDINQPKIKGMRVSTILRFWQFVAIYAIKEFSK
NPMLCCCVLADVMGRGKTWTLTGY
LVDHATYEPDKPTLIICPPHLVWOWASEIKKFTS
KLKILVYFGDAREEPPVPVQALKT
LSSRISDRLHLTQGGDIILDTAWWS"

exon      complement(137703..1377 /locus-tag="An14g05710"
67)
          /number=1
intron    complement(137768..1378 /locus-tag="An14g05710"
24)
          /number=1
exon      complement(137825..1379 /locus-tag="An14g05710"
99)
          /number=2
intron    complement(138000..1380 /locus-tag="An14g05710"
77)
          /number=2
exon      complement(138078..1382 /locus-tag="An14g05710"
98)
          /number=3
intron    complement(138299..1384 /locus-tag="An14g05710"
36)
          /number=3
exon      complement(138437..1385 /locus-tag="An14g05710"
30)
          /number=4
gene      <139122..>140458 /locus-tag="An14g05720"
mRNA      join(<139122..139252, /locus-tag="An14g05720"
139343..139427,
139649..139772,
139813..139963,
140010..140120,
140192..140244,

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140337..>140458)
CDS      join(139122..139252, /locus-tag="An14g05720"
139343..139427,
139649..139772,
139813..139963,
140010..140120,
140192..140244,
140337..140458)

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/product="hypothetical protein"
/protein-id="CAK42133.1"
/db-xref="GI:134081878"
/translation="MPYFAVKGKNSFVDESQGL
APVPSAYRSDKCDMMHAILDLNQR
TCSTHQRPSPSTRAVRVPWFHRTSHEAVEYNITV
TAATSTVSGSFRSLGAHPILILRQ
YDALQGHILYDRGSGQLTSMQACYSRARRHPTSP
IDNHHTAHNEEKGDITLPIDIDFN
YQNTLYLHPLTLVLIGVARHYGENSGQVFLRRQF
HRARKERKWDGGEKSRKMGWMMWEE
VELVSWRNGMEGFRGESAKSMYALARWIIRLHRF
MARHLY"
exon      139122..139252      /locus-tag="An14g05720"
intron    139253..139342      /number=1
exon      139343..139427      /locus-tag="An14g05720"
intron    139428..139648      /number=2
exon      139649..139772      /locus-tag="An14g05720"
intron    139773..139812      /number=3
exon      139813..139963      /locus-tag="An14g05720"
intron    139964..140009      /number=4
exon      140010..140120      /locus-tag="An14g05720"
intron    140121..140191      /number=5
exon      140192..140244      /locus-tag="An14g05720"
intron    140245..140336      /number=6
exon      140337..140458      /locus-tag="An14g05720"
gene      complement(<140647..>14 /locus-tag="An14g05730"
2006)
mRNA      complement(join(<140647 /locus-tag="An14g05730"
..141004,
141055..141527,
141590..141657,
141707..141743,
141796..141815,
141865..141876,
141952..>142006))
CDS      complement(join(140647. /locus-tag="An14g05730"
.141004,141055..141527,
141590..141657,
141707..141743,

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141796..141815,
141865..141876,
141952..142006))

/inference="similar to AA
sequence:UniProtKB:AF119672.1"
/note="unnamed protein product;
Function: PTH11 of *M. grisea* is
required for appressorium
differentiation in response to
inductive surface cues. Function:
as do most fungal plant pathogens,
M. grisea differentiates an
infection structure specialized
for host penetration called the
appressorium. Phenotype: *M. grisea*
cells null mutant for PTH11 are no
more pathogenic. Similarity: the
length of the predicted ORF is
only one half of the *M. grisea*
PTH11. Title: similarity to
integral membrane protein PTH11 -
Magnaporthe grisea"
/citation=[63]
/codon-start=1
/protein-id="CAK42134.1"
/db-xref="GI:134081879"
/translation="MTVSHPKDVLNTINFVTQCV
EDWSCLTAWVLFMGYCGIAIAVGH
YGGGYHIDDVSEAHQVLFKFCYIATVLYCFMAL
FVKIALLSLIRIFNPYRSKIYFI
YGLGCLCIYYIVAEIVKIRMDPVPAYWTQDPK
ARCLNQRAALIADSVISVVTDFII
LILPLPLTWSLQMSRNKKLRVIGMLSAGGLATAF
SLYRLVLVLRDGGSRDQTIIVFMIV
ILSGNAEGGVAMICACLPVTNINILNKLKKEYSS
QRYYPESVSNLSKLGSNKRFSL
GNSRRADGTESASDQSHLITFAGTVDMAGGNDTG
GIHKTVDVSTIEMVADGDSHESH HHGSFH"
/locus-tag="An14g05730"

exon	complement(140647..141004)	/number=1
intron	complement(141005..141054)	/locus-tag="An14g05730"
exon	complement(141055..141527)	/number=1
intron	complement(141528..141589)	/locus-tag="An14g05730"
exon	complement(141590..141657)	/number=2
intron	complement(141658..141706)	/locus-tag="An14g05730"
exon	complement(141707..141743)	/number=3
intron	complement(141744..141795)	/locus-tag="An14g05730"
		/number=4

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exon      complement(141796..1418 /locus-tag="An14g05730"
15)
intron    complement(141816..1418 /locus-tag="An14g05730"
64)
exon      complement(141865..1418 /locus-tag="An14g05730"
76)
intron    complement(141877..1419 /locus-tag="An14g05730"
51)
exon      complement(141952..1420 /locus-tag="An14g05730"
06)
gene      complement(<142716..>14 /locus-tag="An14g05740"
3896)
mRNA      complement(join(<142716 /locus-tag="An14g05740"
..142868,
142941..143171,
143244..143322,
143423..143759,
143845..>143896))
CDS       complement(join(142716. /locus-tag="An14g05740"
.142868,142941..143171,
143244..143322,
143423..143759,
143845..143896))

/codon-start=1
/product="hypothetical protein"
/protein-id="CAK42135.1"
/db-xref="GI:134081880"
/translation="MEEELSGLTRAVVRQQTDPL
PNEGDRWSLTGCWNPTRVSRTEI
GWEGRAEPWEVEVYPRSLHRTTIDYTLQFSLRPL
RVSEFFVDPFLYMQRVANRVGFKP
FCSLADRAQGRRLLEAQESFNSSHLRQRDGSHT
LHSTHSKRKSKFFIAALGVYNNPR
QGQQRAGQACELRGSILPGLTGSMIVCRSPRHH
LFTDAASQPTFQRSPLCRIPYCG
LARTRRSLIPHSGPWVRVVRGAIGTSARGGSNNRRW
LLLLVISIVRSRYFRRPAAMSPRL ARGGGI"

exon      complement(142716..1428 /locus-tag="An14g05740"
68)
intron    complement(142869..1429 /locus-tag="An14g05740"
40)
exon      complement(142941..1431 /locus-tag="An14g05740"
71)
intron    complement(143172..1432 /locus-tag="An14g05740"
43)
exon      complement(143244..1433 /locus-tag="An14g05740"
22)
intron    complement(143323..1434 /locus-tag="An14g05740"
22)
exon      complement(143423..1437 /locus-tag="An14g05740"
59)

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intron	complement(143760..143844)	/number=4 /locus-tag="An14g05740"
exon	complement(143845..143896)	/number=4 /locus-tag="An14g05740"
gene mRNA	<143978..>145355 join(<143978..144235, 144298..144933, 144984..>145355)	/number=5 /locus-tag="An14g05750" /locus-tag="An14g05750"
CDS	join(143978..144235, 144298..144933, 144984..145355)	/locus-tag="An14g05750"

/EC-number="1.3.1.42"
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 /inference="profile:PFAM:PF00724"
 /inference="similar to AA
 sequence:UniProtKB:AF293653.1"
 /note="unnamed protein product;
 Catalytic activity: OPR3 of A.
 thaliana catalyzes the reaction:
 8-[(1R,2R)-3-Oxo-2-[(Z)-pent-2-enyl]
 cyclopentyl]octanoate + NADP+ =
 (15Z)-12-Oxophyto-10,15-dienoate +
 NADPH. Phenotype: A. thaliana OPR3
 null mutants are male-sterile due
 to defects in pollen release
 caused by a delay in the stomium
 degeneration program. Remark:
 Jasmonic acid (JA) and its
 precursor 12-oxophytodienoic acid
 (OPDA) act as plant growth
 regulators and mediate responses
 to environmental cues. Title:
 strong similarity to
 12-oxo-phytodienoate reductase
 OPR3 - Arabidopsis thaliana"
 /citation=[71]
 /citation=[75]
 /codon-start=1
 /protein-id="CAK42136.1"
 /db-xref="GI:134081881"
 /db-xref="GOA:A2R3W8"
 /translation="MTIVQAQGADSKLFQPLAIA
 NGKLTLSHRVVHAPLTRNRGEPLN
 SNSIPENPNRIWYPGDLVVVEYYQRATPGGLIIS
 EGIPPSLESNGMPGVSGLFTEEQA
 AGWKRVVDIVHAQGGYIYCOLWHAGRAIVPQMTG
 YPPVSASASVWDDPEERYTHPAVG
 DSEPVRYSDHPIELTVAHIKQTIQDYCKAAKTA
 MDIGFDGVELHSGNGYLPEQFLSS
 NINRRTDDYGGTPEKRCRFVLELMDELAQTVGQE
 NLAIRLTPFGLYNQARGEQRVETW
 TYLCESLKQAHPHLSYVSFVEPRYEQIHSYEEKD
 AFLRSWGLSSVDLSSFRKIFGSP
 FFSAGGWDQTNWGVLEAGKYDALLYGRYFTSNP
 DLVERLRKGIPFAPYDRTRFYGPF
 EDSAFHYVDYEPAPQNSTGTQESVNVSVRL"
 /locus-tag="An14g05750"
 /number=1
 /locus-tag="An14g05750"

exon	143978..144235	/locus-tag="An14g05750"
intron	144236..144297	/locus-tag="An14g05750"

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exon      144298..144933      /number=1
                                         /locus-tag="An14g05750"
intron    144934..144983      /number=2
                                         /locus-tag="An14g05750"
exon      144984..145355      /number=2
                                         /locus-tag="An14g05750"
gene      complement(<145510..>14 /number=3
6577)      /locus-tag="An14g05760"
mRNA      complement(join(<145510 /locus-tag="An14g05760"
..145699,
145751..145803,
145854..145876,
145933..146045,
146099..146459,
146529..>146577))
CDS       complement(join(145510. /locus-tag="An14g05760"
.145699,145751..145803,
145854..145876,
145933..146045,
146099..146459,
146529..>146577))

/EC-number="1.1.1.245"
/inference="profile:COGS:COG1028"
/inference="profile:PFAM:PF00106"
/note="unnamed protein product;
Catalytic activity: chnA of
Acinetobacter catalyzes the
reaction: Cyclohexanol + NAD+ <=>
Cyclohexanone + NADH. Similarity:
the gene model structure is
confirmed by A. niger EST
EMBLEST:BE759160, which covers
exons 1 to 3. Title: strong
similarity to cyclohexanol
dehydrogenase chnA - Acinetobacter
sp"
/citation=[72]
/codon-start=1
/protein-id="CAK42137.1"
/db-xref="GI:134081882"
/db-xref="GOA:A2R3W9"
/translation="MACKVSGTAFITGGNGIGK
TTAFALAQNGIEAVSLLDVNESLL
QRTKDELATSHPQVAVELTVGDVSKAEACVDEAVR
RTVERFGRIDISVHCAGIVGQPSA
THELTAAEWQVRVIDINQTVLLCQKAVIRQMLTQ
ESRGLRLGRGTIVNVASMFVGVAP
GGWSGLSAYTASKHAVVAFVSKMDAKAYIQQEIRI
NAICPGYTDMDIRTYWDAGYMPV
DSQRVAIGRRQAPEEIAVLFLASPMSSYMVGS
ALVVDGGYTA"
exon      complement(145510..1456 /locus-tag="An14g05760"
99)
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intron    complement(145700..1457 /locus-tag="An14g05760"
50)
                                         /number=1
exon      complement(145751..1458 /locus-tag="An14g05760"
03)
                                         /number=2
intron    complement(145804..1458 /locus-tag="An14g05760"

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53)

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intron complement(145877..145932) /number=3 /locus-tag="An14g05760"

exon complement(145933..146045) /number=3 /locus-tag="An14g05760"

intron complement(146046..146098) /number=4 /locus-tag="An14g05760"

exon complement(146099..146459) /number=4 /locus-tag="An14g05760"

intron complement(146460..146528) /number=5 /locus-tag="An14g05760"

exon complement(146529..146577) /number=5 /locus-tag="An14g05760"

gene complement(<147404..>147784) /number=6 /locus-tag="An14g05765"

mRNA complement(<147404..>147784) /locus-tag="An14g05765"

CDS complement(147404..147784) /locus-tag="An14g05765"

/note="unnamed protein product;
Title: strong similarity to EST
an-3120 -Aspergillus niger"
/codon-start=1
/protein-id="CAK42138.1"
/db-xref="GI:134081883"
/translation="MSIGKIIIGKIIIPILVIIF
ICVCIYFLIKHRRDRKRERREDNL
RAQYIYRQQFQQQYMPHTQMPPQQQQQPGTPAP
PYYNHAYAVGQQQPVAMNEGEYGS
ESMMKKPEPVVYPVQQQHPGSEVV"

exon complement(147404..147784) /locus-tag="An14g05765"

gene <149275..>150765 /number=1 /locus-tag="An14g05780"

mRNA join(<149275..150089,
150140..150471,
150521..>150765) /locus-tag="An14g05780"

CDS join(149275..150089,
150140..150471,
150521..150765) /locus-tag="An14g05780"

/EC-number="1.-.-"
/inference="profile:PFAM:PF01222"
/inference="similar to AA
sequence:PIR:S64014"
/note="unnamed protein product;
Function: the S. cerevisiae ERG4
gene encodes sterol C-24(28)
reductase which catalyzes the
final step in the biosynthesis of
ergosterol. Remark: ergosterol is
the precursor of vitamin D2.
Title: strong similarity to sterol

C-24 reductase Erg4 -
 Saccharomyces cerevisiae
 endoplasmatic reticulum"
 /citation=[6]
 /citation=[18]
 /citation=[22]
 /citation=[54]
 /citation=[66]
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 /protein-id="CAK42139.1"
 /db-xref="GI:134081884"
 /db-xref="GOA:A2R3X1"
 /translation="MKQSKDRSPEGTSNAHEDEK
 PTFEFGGAPGVITMLMLGFPLLMY
 MFIGATLYDGHLPDENQSIDFLSHLVDLAHT
 HAYPNRKAWIIYWTFLVLEGLGYL
 YLPGVYKGKCLPHLNGKQLDYYCSAASSWYVTI
 AALVLHFGIFRLSTLVEEFGPL
 MSVAICSGFLVSI IAYVSALLGAQHRMTGSHVY
 DFFMGAEINPRLFQWLDMMKFEEV
 RIPWYILFLLTLGTALKQWEDYGFVSGEVSFLLL
 AHFLYANACAKGEELIITSWDMYY
 EKWGFMLIFWNLAGVPMSYCHCTLYLASHDPSTY
 KWNPIALGVLFVMIYIFAYVWVWDTIC
 NSQKNLFRQERGGKPVNRKTFPQLPWKSVKNPVC
 IKTKTGDSILCSGWYGMARKVHYS
 CDWFFAFSWGLITGFNSFPWFYSCFFTVMIIHR
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 3445)
 mRNA complement(join(<151141 /locus-tag="An14g05790"
 ..151564,
 151613..151848,
 151899..152339,
 152378..152673,
 152720..153109,
 153190..153256,
 153395..>153445))
 CDS complement(join(151141. /locus-tag="An14g05790"
 .151564,151613..151848,
 151899..152339,
 152378..152673,
 152720..153109,
 153190..153256,
 153395..153445))
 /inference="profile:PFAM:PF04082"
 /note="unnamed protein product;
 Similarity: the predicted protein
 shows similarity to several
 putative and described fungal
 transcription factors; their

exon 149275..150089

intron 150090..150139

exon 150140..150471

intron 150472..150520

exon 150521..150765

gene complement(<151141..>15
3445)

mRNA complement(join(<151141 /locus-tag="An14g05790"
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151899..152339,
152378..152673,
152720..153109,
153190..153256,
153395..>153445))

CDS complement(join(151141. /locus-tag="An14g05790"
.151564,151613..151848,
151899..152339,
152378..152673,
152720..153109,
153190..153256,
153395..153445))

common feature is the presence of a typical binuclear cluster zinc-finger, responsible for DNA binding, which is not well conserved in the predicted protein. Title: weak similarity to transcription activator prnA - *Aspergillus nidulans*"
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RHNAMNRSAGAQSPAQLNQTLTLPVDL
VVAVVKVKKSQPPFFLVSQSWLDSTRVEHLQ
QSIYFPLDPVPPGSLTLFYGILFYVIR
DYLHAGDPDLAHFDLQLSLELCERHFVAGLSK
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ETDVORCWTFLSLAFNMCSIGLHRRSTLEKDE
FAIAEAKRHAFWALYITDKNISLNI
GVTSHFQDHDIDADLYAPSNPKYRFPWDLML
GLVIVEFANVQGRVYDQLYSTISACRADD
EQRSAIERLSSDLMTVRDKLLAIDVSRGLYAD
SLHGMAACADFIAYSVLTVIYRAQT
HPRDVMMAVSSQCYASATAALQSHLKCFYFR
GRQTHKQTEYVNVWILLYPSTPFVIVF
THAITTASTADLALLQDTASSLELIKLSRGS
SMHLYTICDAFVRAAQILVNSQOTLTG
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LSFDPNSDSI"

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		/number=2
exon	complement (151899..152339)	/locus-tag="An14g05790"
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exon	complement(153395..153445)	/locus-tag="An14g05790"
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		/locus-tag="An14g05800"
CDS	154037..156562	/gene="aguA"
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		/inference="similar to AA
		sequence:UniProtKB:ANI290451.1"
		/note="Function: hydrolysis of
		alpha-D-1,2-(4-O-methyl)glucuronos
		yl links in the main chain of
		hardwood xylans. Gene-ID: aguA"
		/citation=[58]
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		aguA-Aspergillus niger"
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		RDINVPELDPPDGFWLQSEGDVTRILGKDARGALY
		GAYEYLAMVAQRNFSRVAYATSPH
		APIRWVNQWDNMDGSIERGYGGASIFFKDGIVVE
		DMAPVEQYARLLASIRINAIIVNN
		VNANATLLLPENMKGLSRIADACRPYGVQIGISL
		NFASPEALGGLNTYDPLDPGVIAW
		WQNIITDSLITYVPDMAGLVKADSEGPDPDTYN
		RTLQQGANLAFARALQPYGGVLMYR
		AFVYDDNLNEDWKADRAKAAVEYFKDLDGQFEE
		NVVIQIKYGPIDFQVREPTSPLFA
		NLYHTNTAIELEVSQEYLQQQCHLVYLPPLWKTV
		LDFDLRVDHKPSMVRDIIISGRFN
		RTLGGWAAVVNVGTNRTWLGSHLAMSNLAYGRL
		AWSPTDESEQILEDWTRLTFGQNH
		HVINTISDMSTSWPAYENYTGNLGIQTLTDILY
		THYGPNPATQDNNWGQWTRADHD
		SVGMDRTIWNGTGYTGQYPEEVARVYESLESTPD
		DLVLWFHHVPVTHRLHSGVTVIQH
		FYNAHYAGAEAAHGFEVRQWESLEGLIDRERYEAM
		RSRLVYQAGHSIVWRDAINNFYYN
		MTGIPDVAGRVGHPWRIEAESMGLDGYQTYTVS
		PFEAASNTTAAIITTSNNTGTART
		SIKAPSGVYDIGVNYDLYGGQSKWTLSVGDKVV
		GQWLGDMEHNSLGHTPSIYLGHS

sig-peptide	154037..154096	ATRITFHVGIRQGDQLKIVGEANGVEPAPLDYI VLLPPGLVD" /gene="aguA" /locus-tag="An14g05800" /inference="protein motif:SignalP:2.0" /gene="aguA" /locus-tag="An14g05800" /product="alpha-glucuronidase aguA-Aspergillus niger" /gene="aguA" /locus-tag="An14g05800" /number=1 /locus-tag="An14g05810" /locus-tag="An14g05810" /locus-tag="An14g05810" /EC-number="2.3.1.48" /inference="profile:COGS:COG5076" /inference="profile:PFAM:PF00439" /inference="similar to AA sequence:PIR:S28051" /note="unnamed protein product; Complex: GCN5 of S. cerevisiae is a component of the SAGA complex, which possesses histone acetylation function and is important for transcription in vivo. Function: GCN5 of S. cerevisiae and many other organisms acetylates histones H3 and H4 non-randomly at specific lysines, causing chromatin remodelling during transcriptional activation. Similarity: in the C-terminal part of the protein there is a bromodomain, which function may be to tether type A histone acetyltransferase to the chromatin during gene activation. Title: strong similarity to histone acetyltransferase Gcn5 - Saccharomyces cerevisiae nucleus" /citation=[21] /citation=[23] /citation=[29] /citation=[31] /citation=[34] /codon-start=1 /protein-id="CAK42142.1" /db-xref="GI:134081887" /db-xref="GOA:A2R3X4" /translation="MDGAELQSPLLDNGQPPLVA KRVTSEEPNAAADAKRLKTSDDRE APPQTNLPAAIRIVFPPEKPAVVEERNCEIEFRV VNNDGSTESTVILTGLKNLFQKQL PKMTKDYIARLVYDHTLSLAICKMPLEIIGGIT FREVRHRRFAEIVFCAASSDQQVK GYGAHLMAHLKDYVRATSPVMHFYTYADNYATGY FQKQGFTKEITLDSKIWMGYIKDY EGGTLMQCSMLPRIRYLEVGRMLLKQACVLAKL
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exon	154037..156562	
gene	<157327..>158616	
mRNA	join(<157327..157515, 157564..>158616)	
CDS	join(157327..157515, 157564..158616)	

exon 157327..157515
 intron 157516..157563
 exon 157564..158616
 gene <159715..>163074
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 160785..160893,
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 162857..>163074)
 CDS join(159715..160332,
 160378..160543,
 160593..160722,
 160785..160893,
 160962..162768,
 162857..163074)

RPLSRNHIVHPPPPQWANGIVTLI
 DPLSIPAIRATGWSPPMDDELARQPRHGHFNELR
 RFLSKIQAHHQAWPFLSPVKNDEV
 PDYYNFIESPMDLSTMEERLENDTYSTPKELIND
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 /inference="profile:PFAM:PF01301"
 /inference="similar to AA
 sequence:UniProtKB:A00968.1"
 /note="unnamed protein product;
 Catalytic activity: hydrolysis of
 terminal,non-reducing
 beta-d-galactose residues in
 beta-d-galactosides. Function:
 cleaves beta-linked terminal
 galactosyl residues from
 gangliosides, glycoproteins, and
 glycosaminoglycans. Remark:
 beta-galactosidase of *A. niger* has
 been already patented under
 patentnumber WO9010703 and
 WO9716555-A1. Similarity: belongs
 to family 35 of glycosyl
 hydrolases. Similarity: the
 absence of nice BLASTN
 alignments,demonstrates that the
 predicted ORF is just an homologue
 of the already described
 beta-galactosidase of *A. niger*.
 Title: strong similarity to
 beta-galactosidase lacA -
Aspergillus niger
 extracellular/secretion proteins"
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 VSGGGFPGWLKRVQGRKTTDQGY
 LDAITPYMQAIGRIIAKAQITNGGPVILFQPENE
 YTACVQDEGYTQKEYMAYVEEQYR
 KAGIVVPFIVNDADPMGNFAPGTGAVDIYSFD
 DYPLQWSTAPSNFNSWSSLSLPL
 SYNETVHEEQSPTTPFSISEFQGGVDPDAWGGVGI
 ETSAAAYIGPEFERIFYKINYGFRA
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 DRQVIREKYSSELKQSNFLQASSA
 YLETHSDNGSYGIYTDATSLAVTRLAGNPTNFYV
 VRHGLTSRESTSYKLRVNTSAGN
 LAIPQLSGSLSLHGRDSKIHLDVYNVGNVSLIYS
 TAEFLTWKQAGSKSVVVLVGGEDE
 LHEFAVPANKGKPTSIEGDGLVQQINSTTVIQW
 AVQPSRRVHFSDTLEVHLLWRNE
 AYNWVLDLPVPGAIGRHVRSHTNRSVIVKAGY
 LLRTAEIIIGTSLYLTGDINTTTTI
 ELISAPQPVTSILFNKNRIPTTITSPGRLTGTLT
 YHKPNISLPDLTTLDDWYYLNTLPE
 VHDPTYDDHLWTPCTHTTTANPRNLTTPTSLIYS
 DYGNGGTLTYRGTFATGNETSL
 YLLTEGGYAYGHSIWLNNITFLASWPGNPAFLSN
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 GNDENFPANGFEMKDPRGILDYTLHGRDDKSAIS
 WKMTGNFPGGESYADLSRGFLNEGA
 LFAERKGYHLPAPTEQWTKRSPFDGLPDERPG
 VGGFATKFDLQIPDGYDVPISVVF
 ENSIMAGDGSGBPFRSELFVNGWQFGKYVNHIG
 PQLSYVPVEGILNNGSNLYALTI
 WAMDEKSFKLDGLRLQANAVVQSGYRKPSLVKGE
 VYKERVDSY"

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mat-peptide	join(159769..160332, 160378..160543, 160593..160722, 160785..160893, 160962..162768, 162857..163071)	/locus-tag="An14g05820"
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intron	160723..160784	/number=3 /locus-tag="An14g05820"
exon	160785..160893	/number=3 /locus-tag="An14g05820"
intron	160894..160961	/number=4 /locus-tag="An14g05820"
exon	160962..162768	/number=4 /locus-tag="An14g05820"
intron	162769..162856	/number=5 /locus-tag="An14g05820"

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exon      162857..163074      /locus-tag="An14g05820"
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5037)
mRNA      complement(<163244..>16 /locus-tag="An14g05830"
5037)
CDS       complement(163244..1650 /locus-tag="An14g05830"
37)

                                /note="unnamed protein product;
                                Function: co-expression of het-e
                                and het-c lead to cell death.
                                Function: het-e1 of P. anserina is
                                responsible for vegetative
                                incompatibility. Remark: het-e1 of
                                P. anserina shows also two
                                sequence motifs, a GTP-binding
                                domain and a repeated region that
                                shares similarity with that of the
                                beta-transducin. Remark: the
                                reactivity of the HET-E protein
                                depends on two functional
                                elements, a GTP-binding domain and
                                several WD40 repeats. Similarity:
                                the similarity to het-e1 involves
                                only the N-terminal half of the
                                predicted protein. Title:
                                similarity to beta transducin-like
                                protein het-e1 - Podospora
                                anserina"
                                /citation=[26]
                                /citation=[44]
                                /citation=[69]
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                                KRSRKCYVYLS DIPSGYGEVPLDEQAGSSVEPAR
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                                GEGKASFVRLQEEIIKSSDDHTIF
                                AWNYCDIEQESRYTVLAPSSCTFLKNVVQWTCPR
                                NSGPTYMTNRLGHLQLPVIYRSGS
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                                DYDISRGRVVRVDLGLLETRATTRD
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                                TEYYPRIWDAENHRLRLSSNDST
                                SLETWAAVRLHNSSGRAIGVVFHISPHRRPESTS
                                TFNVHGWICMQTMKPDMTLSQIVD
                                QVIRGCASASAYEYGNHGSCTLALSRRHHMVATN
                                TFVSGNGSETLINVTVANRYAPCT
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CDS        complement(join(166037. /locus-tag="An14g05840"
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166970..167082,
167142..167268,
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/note="unnamed protein product;
Catalytic activity: A. flavus omtB
converts demethylsterigmatocystin
(DMST) to sterigmatocystin (ST)
and
dihydrodemethylsterigmatocystin
(DHDMST) to
dihydrosterigmatocystin (DHST).
Function: A. flavus omtB is a
demethylsterigmatocystin
6-O-methyltransferase involved in
aflatoxin biosynthesis. Remark:
aflatoxins are polyketide-derived
secondary metabolites. Title:
strong similarity to
O-methyltransferase omtB -
Aspergillus flavus"
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DWSDEESRQILSHLAAAMKMGYSK
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17) /locus-tag="An14g05840"

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intron	complement(167083..167141)	/number=3 /locus-tag="An14g05840"
exon	complement(167142..167268)	/number=3 /locus-tag="An14g05840"
intron	complement(167269..167318)	/number=4 /locus-tag="An14g05840"
exon	complement(167319..167516)	/number=4 /locus-tag="An14g05840"
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mRNA	join(<168480..169074, 169128..169245, 169293..169453, 169507..169540, 169597..>170002)	/locus-tag="An14g05850"
CDS	join(168480..169074, 169128..169245, 169293..169453, 169507..169540, 169597..170002)	/locus-tag="An14g05850"

/note="unnamed protein product;
 Function: PTH11 of M. grisea is
 required for appressorium
 differentiation in response to
 inductive surface cues. Function:
 as do most fungal plant pathogens,
 M. grisea differentiates an
 infection structure specialized
 for host penetration called the
 appressorium. Phenotype: M. grisea
 cells null mutant for PTH11 are no
 more pathogenic. Similarity: the
 similarity to PTH11 of M. grisea
 is limited to the N-terminal half
 of the predicted ORF. Title:
 similarity to integral membrane
 protein PTH11 - Magnaporthe
 grisea"
 /citation=[63]
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 IEAFKYTVIAPNFSMVSTTTGKLSVAVFLLRLMG
 QTASPAKRWFLYIFSIISVAWNVL
 AIVAIMGYCRPAEKIWRPEVPGSCFSLKQFLIAG
 ISQASFNADFALTALFPIIIIFS
 VQLPWKKMLGVIAVMGAGILAAAATLVKAILLKS
 LPAHSIDITCEHQIRGAQTHKKKL

NIELQGLGPILQHGTNPNTILSAPLESSGAHPVHR
 QMYVIIICATLPTLRQSYNFALHR
 TRYLGSSYYKGSHSEAAAAAARQKPIPLLRQPD
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 GGAYAPMSGYFLPSNLLDQNGFR
 TPKIIAEGLAVPAGKVGDDSEPVSSAMVTSRMK
 LNQVLGNRRKVGCAASLPAGTAAH
 PVEHGFLAGRSGVGVSFGEAGDPAFEGSYEDDY
 DDACANHAASDGDREDKEALKNGG
 KTDNTGESEYPRFSQVDYFTQHQLQIRTTGLPK
 RPRYSAAATVGFPCTVTWAFIDRG
 DPKHGMPTAADLPWEIRTLHETNELNTIAAYLAS
 MRRNLKOLDVNFTFHYRPVFSFDK
 ADRVKKIGGYSSDKQNAHTVADLYMHTKDDRSW
 GTLCVTRHHVQGMWHYWAIAAI
 SPPKSPFQSVDEKGVYLLMYDSRPLKEPTKKRDR
 DYWRNVMRRDQYKLLVEIGKNFV
 LDLAINRRQLSVEGEDDPLRLTLWWLWNIARYGG
 GFYERDGELEDPRWRLTDARWLHF
 DQDWSNVRTALRWKNVKEWFSEQRLEQLTHEQ
 RIQAHAVAA"

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		/number=1
gene	<172769..>173936	/locus-tag="An14g05870"
mRNA	join(<172769..172958, 173013..173080, 173134..173513, 173575..173639, 173698..>173936)	/locus-tag="An14g05870"
CDS	join(172769..172958, 173013..173080, 173134..173513,	/locus-tag="An14g05870"

173575..173639,
173698..173936)

/note="unnamed protein product;
Function: PTH11 of *M. grisea* is
required for appressorium
differentiation in response to
inductive surface cues. Function:
as do most fungal plant pathogens,
M. grisea differentiates an
infection structure specialized
for host penetration called the
appressorium. Phenotype: *M. grisea*
cells null mutant for PTH11 are no
more pathogenic. Similarity: the
length of the predicted ORF is
only one half of the *M. grisea*
PTH11. Title: similarity to
integral membrane protein PTH11 -
Magnaporthe grisea"
/citation=[63]
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VLMGIGLFFSYGLTLCVISAFNGVGHEFWSLSR
PTRGTVILLFWCSTKFWVLSHV
KFSYIVLLRRKLFGAITYWRRLTALIVFTLAWGI
ASIFVSIFQCWFPVRYFWIKHIDGS
CMQGRNTFYIVVGSIALAENFILVSMPLVVVWGM
NLSRQKVELSLIFGFGGLVCAIG
LLRMVTFKRYVTADATNGYLQAIWSIVELELGI
ICASVILMRPIFPPLGIQNEML
HHAWPNIKVQLFKRRADDEFVVMABEAGLCRDG
ISG"

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exon	173013..173080	/locus-tag="An14g05870" /number=2
intron	173081..173133	/locus-tag="An14g05870" /number=2
exon	173134..173513	/locus-tag="An14g05870" /number=3
intron	173514..173574	/locus-tag="An14g05870" /number=3
exon	173575..173639	/locus-tag="An14g05870" /number=4
intron	173640..173697	/locus-tag="An14g05870" /number=4
exon	173698..173936	/locus-tag="An14g05870" /number=5
gene	<175066..>176514	/locus-tag="An14g05880"
mRNA	join(<175066..175356, 175420..175941, 176025..176078, 176188..>176514)	/locus-tag="An14g05880"
CDS	join(175066..175356, 175420..175941, 176025..176078, 176188..176514)	/locus-tag="An14g05880"

		/inference="similar to AA sequence:UniProtKB:NCB912.2" /note="unnamed protein product; Similarity: the central part of the predicted ORF shows only weak similarity to N. crassa B912. 20. Title: strong similarity to hypothetical conserved protein B912.20 - Neurospora crassa" /codon-start=1 /protein-id="CAK42149.1" /db-xref="GI:134081894" /translation="MPLASDAFQADLSRLSPSHL EVSLPVTLSLAVLAYLLVSTLRF QRVRILYRDYPQYTTRASMSQMTVDDAWAIQKNI LQLEFPITTAVKALQFALFRTYGIP TISSLLHTSQFSNPATSKRYADIGALIGQFVT CPPTSSRRTAIAITKFLHSGYRA SGRILESDMLYTLSLFATEPIRFVERFEWRAMTE LERCAIGTYWKSGLDALDISYDEL PSGKSGFSDGLHFLEELRQWGDHYEENMRPDHR NRLVADKTMDEVIVYGFPKWHILCD GFCKEPCADSLNQEVFSDTPNEDGRYYVQIWKGM PYYVQPTMNNRWGPAAMLTNALGL PLPGDDGDTYYPRGFDVADLGPQFEGRGRKSVG EYVDVLEKEHKQCPFGGRSDQPE ICLSR" /locus-tag="An14g05880" /number=1 /locus-tag="An14g05880" /number=1 /locus-tag="An14g05880" /number=2 /locus-tag="An14g05880" /number=2 /locus-tag="An14g05880" /number=3 /locus-tag="An14g05880" /number=3 /locus-tag="An14g05880" /number=4 /locus-tag="An14g05890" /locus-tag="An14g05890" /locus-tag="An14g05890" /EC-number="5.2.-.-" /inference="profile:COGS:COG4716" /note="unnamed protein product; Remark: CLA compounds(cis,trans)-9,11-linoleic acid and (trans, cis)-10,12-linoleic acid are recognised nutritional supplements and effective inhibitors of epidermal carcinogenesis and forestomach neoplasia; furthermore CLA has also been shown to prevent adverse effects caused by immune stimulation in chicks, mice and rats, and has been shown to decrease the ratio of low density lipoprotein cholesterol to high
exon	175066..175356	
intron	175357..175419	
exon	175420..175941	
intron	175942..176024	
exon	176025..176078	
intron	176079..176187	
exon	176188..176514	
gene	<176803..>178484	
mRNA	join(<176803..177362, 177419..>178484)	
CDS	join(176803..177362, 177419..178484)	

density lipoprotein cholesterol.
 Remark: the linoleate isomerase is used in a method for producing conjugated linoleic/linolenic acid (CLA) from oils such as sunflower oil, safflower oil, corn oil, linseed oil, etc. Similarity: the N-terminal part of the prediction ORF shows also weak similarity to some oxidoreductases. Similarity: the patented protein, as well as the predicted ORF, show strong similarity to the 67 kDa myosin-crossreactive streptococcal antigen of *Streptococcus pyogenes*, a protein with unknown function, but involved in the pathogenesis of streptococcal infections.
 Title: strong similarity to linoleate isomerase protein sequence PCLA591 from patent WO9932604-A1 -*Lactobacillus reuteri*"

/citation=[19]
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 PPSRVHILETLQAGGGSISTGDPVNGYDCRAG
 MPPFNDVCMEEILLSVPSKTNPNL
 TVLEEFHEFWDTAVKDHPTFLTRHKHGLERI
 DAKRASLGLRDRVDLFMLASKSDK
 SLGRSRICDHFNSFFKSYYWMLLSTTFGIKPVH
 SAAEFRRYLQHYMHDIHEIHCRRK
 LDGGRYNRHESIVPIAHFLCSRGVDFRFHTT
 DIITPSSSEPHRVSAIKAIHENE
 PEMTINLGERDIVLVSLGSMGSGTTGTNTSPPS
 LELMDIEKDLDENWLLWLELSTKN
 PIFGNAYNFCTRMAESRLESFTVFSSPEFFNRF
 TALTDKVGSGTFVTLKDTPLL
 INLPQQFLFPDQFAHVQVLWGYAMYPERE
 GDIYK KPMLECSGQEIEMEEILKQLNFPVQ
 GILDHSITLPCVVPRAAATLLVRLRSDRPPV
 IPIDNLGLIGQFVDIPGEVAVTMDY
 GVRSAQTAVRQLMGLERHKVLSKRSSAINLKAL"

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intron	177363..177418	/locus-tag="An14g05890"
		/number=1
exon	177419..178484	/locus-tag="An14g05890"
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gene	complement(<179356..>181260)	/locus-tag="An14g05900"
mRNA	complement(join(<179356..179403, 179482..>181260))	/locus-tag="An14g05900"
CDS	complement(join(179356..179403, 179482..181260))	/locus-tag="An14g05900"

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/inference="profile:COGS:COG3122"
/inference="similar to AA
sequence:PIR:T49456"
/note="unnamed protein product;
Similarity: other BLASTP hits are
explained by the relatively high
content of low-complexity regions.
Title: strong similarity to
hypothetical protein B14D6.80 -
Neurospora crassa"
/codon-start=1
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IDLSAFTYDNPIEQPAKRRRLSHEITPVKDVPLP
PAKNSLFLFSDDDIILSSDGFAPT
KPPAWNNGESDP IVFTSSAPEPTHNLFPVRPAISSR
AVNTISLDDDDAGNSSDTRSNNRP
RKEAIQVSSDQLDFPDVDDLVAQRVEANAFSS
RTANLLATLEDRSRGNSGESASRS
SRGRRIQDQSDDIEVEEMPPPRKQPKAKIKVTSE
EKEAKAREREA AKAQREHQRLEK
ERKQKAKEDKAREKQLAADIAEVNKLKVKDKDST
HEMLIDLASTFTDTS LGNQTSELM
RLLKVDLSFFPSTIPNIVKWRRKVRATYNDLSLGH
WEPALHIRDEEEHVLCIIAAQDF
INMIVAPTTEPRNTINDHVERLKLAYPKSRPIYL
IEGLTSLMRKNNNAQNRAYQAAVR
RQYEDSSARPSTRKQQQPEFVTPIDSDTVEDAL
LDLQVTHSLCIHHTSSPAESAEWI
KNFTEYISTVPYRRERMDLNSAF CMDVGQVKPG
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IATQYPSAMDVLNAMRKHGPGLLEDVKQTKTAPS
PIHALVQP"

exon      complement(179356..1794 /locus-tag="An14g05900"
03)

intron    complement(179404..1794 /locus-tag="An14g05900"
81)

exon      complement(179482..1812 /locus-tag="An14g05900"
60)

gene      complement(<181479..>18 /locus-tag="An14g05910"
2990)

mRNA      complement(join(<181479 /locus-tag="An14g05910"
..182086,
182177..182601,
182623..>182990))

CDS       complement(join(181479. /locus-tag="An14g05910"
.182086,182177..182601,
182623..182990))

/EC-number="2.4.1.-"
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/inference="profile:PFAM:PF00534"
/inference="similar to AA
sequence:PIR:S64069"
/note="unnamed protein product;
Function: ALG2 of S. cerevisiae is
involved in N-glycosylation,
converting

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man[2]glcnac-pp-dolichol to
man[3]glcnac-pp-dolichol. Title:
strong similarity to
mannosyltransferase Alg2 -
Saccharomyces cerevisiae"
/citation={3}
/citation={15}
/codon-start=1
/protein-id="CAK42152.1"
/db-xref="GI:134081897"
/db-xref="GOA:A2R3Y4"
/translation="MPPAKITIIHPDLGIGGAER
LIIDVALALQSRGHPVTIYTSHRD
KSHCFEEARDGTLDVQVRGNTIFPAHVGGRLEVL
MAILRQLHLTWDLLCGETTSGDNG
EGEEEVFIVDQMPACVPFLKVRKQIRILFYCHFPD
QLLARRDEGGSVLQLLKGLYRVFF
DWFEGWAVSASDKVVSANFRTRGVVSGVFGREKV
GDLSVYPCVDTKAGDGGEGVVKD
GEKLWGGKKILLSVNRFRERKDLALAIRAYHGLG
EEKRKGTRLVVAGGYDNRVQENVQ
YHRELDLATGLGLQTATSKTVISALSIPDSIDV
LFLLSVPTAFRDTLLLOAKLLLYT
PINEHFGIVPVEAMRAGVPLASNTGGPLETIVE
GETGWLRLDAKVDAWTAVMKVLV
GMKQEEELDRMSVAAKERVEKEFSLTAMGEKLEQE
IEEMLGQEQRPFHGFQQLLTFLAL
VGVLALAAAFVLKLL"
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86)
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76)
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01)
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22)
exon      complement(182623..1829 /locus-tag="An14g05910"
90)
gene      complement(<183872..>18 /locus-tag="An14g05920"
9440)
mRNA      complement(join(<183872 /locus-tag="An14g05920"
..184411,
184472..188524,
188581..188756,
188813..189136,
189281..>189440))
CDS       complement(join(183872.. /locus-tag="An14g05920"
.184411,184472..188524,
188581..188756,
188813..189136,
189281..189440))

/inference="profile:COGS:COG5059"
/inference="profile:PFAM:PF00225"
/note="unnamed protein product;
Function: kinesins are
microtubule-dependent motor
proteins, involved in organelle

```

transport, in mitosis and meiosis, and in the transport of synaptic vesicles along axons of animal neurons. Similarity: the closest homologues, comprising XCENP-E of *X. laevis*, are involved in driving congression of chromosomes to the metaphase plate. Similarity: the main feature of the predicted ORF is to contain, in the N-terminal half, several kinesin-like domains, explaining the strong similarity to several different kinesin-like proteins. Similarity: the predicted ORF has just half of the length of XCENP-E of *X. laevis*; the best homologue, having also a corresponding length, is a *N. crassa* hypothetical protein. Title: strong similarity to kinesin-related protein XCENP-E - *Xenopus laevis*"

/citation=[41]
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EDGKTAVKVAVVRVPPKLPKTDPGYELVPQRFQRP
MVHVNTNPTSAIDVPQGRKLFVFD
RVFAETVDDQDGVWDYLSDSVSSFLQGVNVSILAY
GQSGAGKSYTMGTSGPSEQSDPRS
MGIIPRAAQLLEKLEGPAPKPNRNSGTGLRTPSR
YSVGSASSFGKASVEKNWOLKATY
VEIYNQLRDLVPESTHQDGRGTVTIREDAKGR
IILTGLHQVNINSYEDLMGALSFG
SSIRQTDSTAINAKSSRSHAVFSLNLVQRKASNG
VMSPTPKDKRMSMPVDMMSGSDAS
VMVDSKLHFVDLAGSERLKNTGASGERAKEGISI
NAGLAALGKVISQLSSRQAGAHVS
YRDSKLTRLQDLSGGNAYTMIACVNPAEFHL
ETVNTVOYQARARAIQSKPRIQOI
ADESDKHAVIERLKAFAVLRQQLRNAEENGRRS
AAPQDRAERQNEREVELQNQLLDT
QESYNALSQRHAKLISEIARDSEHAGETDPNDVV
SLVGKTSVERLKRQSFASIEQV
VLEYEKTIQSLESSLNTSRSSLSVTESTLLERET
KCAVYETVNSQLQARIQKLLDRES
STETYLHELEARLDGQSTGEEKQAAIVAELRKEL
SRARESEANCEDYISTLEERLAEA
DQDMELMOREMERLEHVIERQRLGKLDNLLEYEL
DHVQNGNQEQSEDELETHVPV
AKGAYKPRTRATSLSLDVLTEAVETAIPESDEGL
TEPAPEAVHEASVEAEATAETDET
NLKVLESATDRLEAQENGARASRASTPTQTQKVVA
DKLETVTQELFDLRMQHESTVSEY
EMLEAKYAEAMKALAEFQORDAADAERHPDEKQVD
LLSTNVESRPVSFLFEEGKAPGSND
GKQPSSSPSLSSELSLAGEPASSHEQSTLSNGEV
PQENHVDTREIDEAKAQVEQMR
LLEMHQEGVSIQKQYQLOQSEHGTLSLIETLK
AELQSKNSSPSTPGFKSPVIRR

KTSQSLIGTVDRAHRS LAALRNIAVEEFEARPDT
 MQNFVHLD SAMH LHNRMER IQA
 LEAENQSVKKEMETKSTII SGLTRRSSLQGGGG
 SSVDMGLVNLQRLQVQVQENLINE
 MKESHDAREQLLAEIEELKSLKTQEEAAKAQD
 LCAEEQERKISSLEGEVTELSKSH
 HNAVESLQSSQEQLSATLAELDKALASIDAMRSE
 QTAAGEASASKDAAARELEAEREQ
 QEELVAKLKHVIDEHKATNAHLEKIASLEKSHG
 EAQLQSELAAKDNDSNEVQVHQ
 SRVSELEKEIDSHKSLADSKFKDLESQESHKQE
 VTELEARATAAAQGDYESRFATMS
 AEHEEAMKTLRSEILESEELTKLLNMVSKLLNA
 DVTAEATMAEQIQEIMAKQHFSDK
 YAEMLDTNEDLRKQLETKGSDEGRL
 EELMQSNSSKEAKVNELALLVATLEDITLLQKEE
 QVKKKEAIIAEVKAKEKSVRLVEELEEQITNSF
 DQHHNRLSVIQQERDQALEDAVK
 IAAEKDIEITYRVRIEQLEIKNQDSSSHDRSSIT
 SNLRKSSSATS LPSPPPIPLPPL
 PTIASATNGTGSISPPSSRHTSKELVNPQIVDDQ
 EARIRITIEKHLNAEKQLTATLEEA
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		/number=3
exon	complement(188813..189136)	/locus-tag="An14g05920"
		/number=4
intron	complement(189137..189280)	/locus-tag="An14g05920"
		/number=4
exon	complement(189281..189440)	/locus-tag="An14g05920"
		/number=5
gene	complement(<190148..>191691)	/locus-tag="An14g05930"
mRNA	complement(join(<190148..190283, 190763..190861, 190948..191206, 191652..>191691))	/locus-tag="An14g05930"
CDS	complement(join(190148..190283, 190763..190861, 190948..191206,	/locus-tag="An14g05930"

191652..191691))

/note="unnamed protein product;
Similarity: the similarity to NAB2
of M. musculus is weak, and the
gene structure of the predicted
ORF is questionable. Title: weak
similarity to NGFI-A binding
protein 2 NAB2 - Mus musculus"
/citation=[25]
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PELQSIRREFWNNFCRQYGNRSSP
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GRPSFSTSHRPLVSTSVQLNIVKR
PTWANAPAQPHPGSLQP"

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exon	complement(190763..190861)	/number=1 /locus-tag="An14g05930"
intron	complement(190862..190947)	/number=2 /locus-tag="An14g05930"
exon	complement(190948..191206)	/number=2 /locus-tag="An14g05930"
intron	complement(191207..191651)	/number=3 /locus-tag="An14g05930"
exon	complement(191652..191691)	/number=3 /locus-tag="An14g05930"
gene	complement(<192418..193985)	/number=4 /locus-tag="An14g05940"
mRNA	complement(join(<192418..192525, 192596..192700, 192794..192853, 192940..193251, 193625..193690, 193783..193884, 193959..193985))	/locus-tag="An14g05940"
CDS	complement(join(192418..192525,192596..192700, 192794..192853, 192940..193251, 193625..193690, 193783..193884, 193959..193985))	/locus-tag="An14g05940"

/note="unnamed protein product;
Similarity: very weak similarity
to a fragment of protein SEQ ID
NO:917 of patent n. WO200042171-A1"

of *Eucalyptus grandis*. Title:
questionable ORF"
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/db-xref="GI:134081900"
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SRPGYNTFIIPSFLPMSLVNKIES
GQNGGTFFDDRYSGADIRACRNNVLAAGEEKLRY
LQKFMQYLSQRRITFGRISLSFGS
LAINEPLNPLWVMVLLIDRSVNRLLGSRYSIIHF
SVLDNKAGRLCCYDDIGIMRFYSW
LQKCITSMEDLVYRIYIVGLVRNLHAMNVMTCLK
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HLWPEVE"

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		/number=1
exon	complement(192596..192700)	/locus-tag="An14g05940"
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intron	complement(192701..192793)	/locus-tag="An14g05940"
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exon	complement(192794..192853)	/locus-tag="An14g05940"
		/number=3
intron	complement(192854..192939)	/locus-tag="An14g05940"
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exon	complement(192940..193251)	/locus-tag="An14g05940"
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		/number=5
exon	complement(193783..193844)	/locus-tag="An14g05940"
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		/number=6
exon	complement(193959..193985)	/locus-tag="An14g05940"
		/number=7
gene	complement(<194969..>196478)	/locus-tag="An14g05950"
mRNA	complement(join(<194969..195817,195865..196221,196455..>196478))	/locus-tag="An14g05950"
CDS	complement(join(194969..195817,195865..196221,	

196455..196478))

/note="Similarity: a short stretch
of amino acids of the predicted
ORF shows some weak similarity to
an A. thaliana hypothetical
protein."

/codon-start=1

/product="hypothetical protein"

/protein-id="CAK42156.1"

/db-xref="GI:134081901"

/translation="MFGTNRDITTPSVLYLTESL
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NPFKSLREQKISVPVLCGPHEQGPDTDHIDIFGQ
EFRTHSSLIKEYTGWIKERQGEY
AERRVHYFEARTEKDGWGIYRKGAVALTPQRY
RDYPEIPDERIPSAIESFHCFLQA
LYLKPVVPYVGKGRMRMVLGIRFQAVPRVREYI
EKIILPWLTSKPLLGLTDDILAY
TKMAQDIQCAQLYRECLIHLVGMAGYWRNEFNH
AEHILTPSYASLIRHVGTOQLI
EKADVALHTFIRTLATQKPRRIPNFFLRQFTDTV
DNITGLNGRNMSLGYYQHRLVL
NDMQLRIPRGSTYNMCHRLWQFIGCLCVNGLLYT
QDQIKGYPCISPTDIELPWLAN
APEAPVEDQVRDAIMEG"

exon complement(194969..1958 /locus-tag="An14g05950"
17)

/number=1

intron complement(195818..1958 /locus-tag="An14g05950"
64)

/number=1

exon complement(195865..1962 /locus-tag="An14g05950"
21)

/number=2

intron complement(196222..1964 /locus-tag="An14g05950"
54)

/number=2

exon complement(196455..1964 /locus-tag="An14g05950"
78)

/number=3

gene complement(<197258..>19 /locus-tag="An14g05960"
8879)

mRNA complement(join(<197258 /locus-tag="An14g05960"
..197342,
197402..197552,
197606..197698,
197751..197968,
198017..198238,
198288..198371,
198435..198525,
198598..198694,
198745..>198879))

CDS complement(join(197258. /locus-tag="An14g05960"
..197342,197402..197552,
197606..197698,
197751..197968,
198017..198238,
198288..198371,
198435..198525,
198598..198694,
198745..198879))

/EC-number="3.5.3.11"

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/inference="profile:COGS:COG0010"
/inference="profile:PFAM:PF00491"
/note="unnamed protein product;
Catalytic activity: H2O + agmatine
<=> urea + putrescine. Complex:
agmatinase of E. coli is a
homodimer of the speB gene
product. Function: agmatinase of
E. coli is part of the second
putrescine biosynthetic pathway;
it also represents the only
pathway for urea biosynthesis in
E. coli as no urease is present.
Similarity: the predicted ORF
shows much stronger similarity to
putative agmatinases of N. crassa
and S. pombe. Title: strong
similarity to agmatinase speB
-Escherichia coli"
/citation=[4]
/citation=[10]
/codon-start=1
/protein-id="CAK42157.1"
/db-xref="GI:134081902"
/db-xref="GOA:A2R3Y9"
/translation="MYLSVVSLALSGIVTAHSS
HDQTPLAGPHQRLWYNTLFGDGGT
QADSVFSGISTFGRLPYFPCLSSAEARYDIAFIG
APFDITGTSYRPGARFGSPGIRQGS
RRNLNLYGGYNVPLQANPFVSDLRVLDGDIPTVS
YDNAWAIQQIEEGHNSVLMRKPF
DAEKYGLSKAGKTLPRITLGGDHTITLPLLRSI
NRAYGPVTVIHFDSDLWSKPKVF
GGSPSQVAAINHGTYFYHAAMEGLLKNDNTIHAG
IRTTLSGSPSDYENDGYCGFEIVEA
REIDTIGTDGIIKKIRERVGTENPVYLSIDITL
DPAYAPATGTPETGGWSTRELRTI
IRGLDGLNFIGADIVEVAPAYDTNAELSTMAAAD
VLYEVLTIMVKKGPLSVGRSDEL"
sig-peptide      complement(198823..1988
79)              /locus-tag="An14g05960"
                  /inference="protein
motif:SignalP:2.0"
mat-peptide      complement(join(197261.
.197342,197402..197552,
197606..197698,
197751..197968,
198017..198238,
198288..198371,
198435..198525,
198598..198694,
198745..198822)) /locus-tag="An14g05960"
exon              complement(197258..1973
42)              /product="unnamed"
                  /locus-tag="An14g05960"
intron            complement(197343..1974
01)              /number=1
                  /locus-tag="An14g05960"
exon              complement(197402..1975
52)              /number=1
                  /locus-tag="An14g05960"
                  /number=2

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intron      complement(197553..1976 /locus-tag="An14g05960"
05)
exon        complement(197606..1976 /locus-tag="An14g05960"
98)
intron      complement(197699..1977 /locus-tag="An14g05960"
50)
exon        complement(197751..1979 /locus-tag="An14g05960"
68)
intron      complement(197969..1980 /locus-tag="An14g05960"
16)
exon        complement(198017..1982 /locus-tag="An14g05960"
38)
intron      complement(198239..1982 /locus-tag="An14g05960"
87)
exon        complement(198288..1983 /locus-tag="An14g05960"
71)
intron      complement(198372..1984 /locus-tag="An14g05960"
34)
exon        complement(198435..1985 /locus-tag="An14g05960"
25)
intron      complement(198526..1985 /locus-tag="An14g05960"
97)
exon        complement(198598..1986 /locus-tag="An14g05960"
94)
intron      complement(198695..1987 /locus-tag="An14g05960"
44)
exon        complement(198745..1988 /locus-tag="An14g05960"
79)
gene        complement(<199830..>20 /locus-tag="An14g05970"
1412)
mRNA        complement(join(<199830 /locus-tag="An14g05970"
..200758,
200827..>201412))
CDS         complement(join(199830. /locus-tag="An14g05970"
.200758,
200827..201412))

/inference="profile:COGS:COG0534"
/inference="profile:PFAM:PF01554"
/inference="similar to AA
sequence:PIR:T37517"
/note="unnamed protein product;
Title: strong similarity to
hypothetical protein SPAC11D3.06 -
Schizosaccharomyces pombe"
/codon-start=1
/protein-id="CAK42158.1"
/db-xref="GI:134081903"
/translation="MYDSLPSYRETSSAHTEEE

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		HTPLLPKQVDPDPDSKSAKSSVSF LVEFFRLKKDSIPVILAYTLQNSLQTTSVLIVGR TSPENLATTAFSLMFAMVTAWMIA LGGTTALDTLASFTTGSSSNKHDLGILLQRAFFV LGLFYVPVAILWTCSEPVFLLLGQ DPQLSRDSARFLTCLIPGGGLGYIYFEAMKKYLQA QGIMRPGTYVLLITVPFNALLNYL FCYITFRMGLLGAPFATGISYWLFSALLVLYARFI AGSECWGGWSRKAFENLGTFFARLA FLGVVHVGTIEWWAFEIIVALAAGR LGTIPLAAQSV IMTADQVLNTIPFGVG VATSSRVG SLLGSRDAAGASRAANTAANWLSMALGGAVLAVLM GTRHVFAKIFNSDEGVVQLTAEVL PWVALFQIADGLNGSCGGS LRGMGRQHV GALVNL ASYYCGALPLGIWLA FNWGLKGL WVGQCIALYLVGALEWTVAFSNWEGEVDKAFQR MDIHDRLEVGHITTINGATTVV" /locus-tag="An14g05970"
exon	complement(199830..200758)	/number=1
intron	complement(200759..200826)	/locus-tag="An14g05970"
exon	complement(200827..201412)	/number=1 /locus-tag="An14g05970"
gene	<202677..>204146	/number=2
mRNA	join(<202677..203229, 203273..203374, 203431..>204146)	/locus-tag="An14g05980"
CDS	join(202677..203229, 203273..203374, 203431..204146)	/locus-tag="An14g05980"

/inference="profile:COGS:COG0477"
 /inference="similar to AA
 sequence:PIR:S61140"
 /note="unnamed protein product;
 Function: TPO3 of *S. cerevisiae* is
 a vacuolar polyamine transporter,
 that controls the cytoplasmic
 spermine content. Phenotype: *S.*
cerevisiae cells in which TPO3 was
 disrupted showed an increased
 sensitivity to polyamine toxicity
 and a decrease in polyamine uptake
 activity and polyamine content in
 vacuoles. Phenotype: *S. cerevisiae*
 cells overexpressing TPO3 were
 resistant to polyamine toxicity
 and showed an increase in
 polyamine uptake activity and
 polyamine content in vacuoles.
 Remark: TPO3 of *S. cerevisiae* is
 also called YPR156c or P9584. 7.
 Similarity: the predicted ORF is
 125 amino acids longer at the
 N-terminus than TPO3 of *S.*
cerevisiae. Title: strong
 similarity to polyamine transport
 protein Tpo3 - *Saccharomyces*
cerevisiae"
 /codon-start=1

exon	202677..203229	/protein-id="CAK42159.1" /db-xref="GI:134081904" /translation="MNLKLTQIDLVPVPEKQSQS DIDSLPVEQHGHTHPAPTSDDLPLD PLNWPRWRKHVILGIVMLKFVLEQSRRTHRLTM NRYFLFTYITTTTVPSPAIEQSQY DINYSQVNNTVAIPALGLSLGPLFWSSVVDIYGR RIVFIVGTVIALVATIGAAVADTY GGYMAARFFQGFVSPSSTVGMVANGTVTDMFY EYERGQKLGLWVLALDSGLLLGPT FGGFLNLVSAQWLNWFNAILFAALLLELTLMPE TLYPRALMLQRMVTEKPAESNAG IEEAGIKRTKSLPFFNLRIPIGLSHPPPIYASLRT FLLTFRFPVIAVAVIGYSFTWYWW ILSVITMVP SAYATD SPLIOGLLFLGLLIGITLVA EVSCSGRLSDAIVGRLAKRNGVR VPEMRLWLAYPAIVLTAGVYIPAHVRTISNIAI QPAVGLILWGISIDKAIYHWMVGQV AFFLCE" /locus-tag="An14g05980" /number=1
intron	203230..203272	/locus-tag="An14g05980" /number=1
exon	203273..203374	/locus-tag="An14g05980" /number=2
intron	203375..203430	/locus-tag="An14g05980" /number=2
exon	203431..204146	/locus-tag="An14g05980" /number=3
gene	complement(<205094..>207843)	/locus-tag="An14g05990"
mRNA	complement(join(<205094..207273, 207361..207431, 207517..207554, 207700..>207843))	/locus-tag="An14g05990"
CDS	complement(join(205094..207273,207361..207431, 207517..207554, 207700..207843))	/locus-tag="An14g05990"

/note="unnamed protein product;
 Title: weak similarity to spindle
 pole body-associated protein sadlp
 - Schizosaccharomyces pombe"
 /codon-start=1
 /protein-id="CAK42160.1"
 /db-xref="GI:134081905"
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 AVDRHSTRVFSRRVAFALGRQLP
 RIAIDTSELVILVAAIVALASPALDCLRLQASY
 SVPSSHTNRNIKPIILLRIELPMPA
 RRGATRAGSTRSDIGSASTYFOSKLGPEARTQA
 LPNLPTKQSFAYGSAETPILPREL
 KIQPHMDLTEMADAIDKGIEDAKDRQMKETKTQ
 DKSRQKSPSITRSPVRRSRREP
 PDELQLLDNLREATKSPTVGRGYNNDQSTATP
 TPPIPHTLTASSPAQSLVPVRY
 HVPANLYPSPMGRFGPQLHDGFPGLGSSPLPDDS
 SLYSFTVERAINSDELTRTLSDGK
 NIKAPPRRFSGLAFANEPHIEEEEPDSRLKTKS
 RSPSLQPSYEDFQIEPSPEPEQSQ
 EPESVQEELEPTPEPEPIPELEPMPEPTPEPEV
 IREKSPAAQFTAPTAKTLIPNAYAR

RTPSQEPSVDDGQQNIRQTGQSWSWVGSLSAQLP
 SVSTVARILAGIALAAATVYLVAF
 GGIPSLSRPPQYIPMDENNMLAVSSSLTDQMSRIG
 AQVSSLAKEMRTVKWDVNEVQSEV
 RSSPTPIMPSPSRGSTD LGPPTQKTNFLSIGLV
 IVIPGLTSP TVGHKL SAWQWAYVN
 LWRGSHYRPASPPLAALVPWEDY GDCWCSTPRDG
 MSQIGIDL GQKIVPEEVAVEHMPK
 TATLKPENAPREME LWAQYVLVQKGTSRPARTQA
 ERF SIHKPIMDALRS AWPTEDPTA
 YSDDPLLGP TY YRVGKFTYDIHGSHHVQRFELDA
 VIDSP EVRVDRVVF RATS NWGGNH
 TCYRLKLF GHV"

exon	complement(205094..207273)	/locus-tag="An14g05990"
intron	complement(207274..207360)	/number=1 /locus-tag="An14g05990"
exon	complement(207361..207431)	/number=1 /locus-tag="An14g05990"
intron	complement(207432..207516)	/number=2 /locus-tag="An14g05990"
exon	complement(207517..207554)	/number=2 /locus-tag="An14g05990"
intron	complement(207555..207699)	/number=3 /locus-tag="An14g05990"
exon	complement(207700..207843)	/number=3 /locus-tag="An14g05990"
gene	complement(<208451..>210658)	/number=4 /locus-tag="An14g06000"
mRNA	complement(join(<208451..208726, 208778..209568, 209634..209834, 209889..210489, 210572..>210658))	/locus-tag="An14g06000"
CDS	complement(join(208451..208726,208778..209568, 209634..209834, 209889..210489, 210572..210658))	

/inference="profile:COGS:COG2319"
 /inference="profile:COGS:COG5635"
 /inference="profile:PFAM:PF00400"
 /inference="similar to AA
 sequence:PIR:S56893"
 /note="unnamed protein product;
 Function: MDV1 of *S. cerevisiae* is
 involved in the mitochondrial
 membrane fission event by
 regulating the assembly of Dnm1p,
 a dynamin-related GTPase, into
 punctate structures at the outer
 mitochondrial membrane. Phenotype:
 the mitochondrial fission is
 blocked in *S. cerevisiae* MDV null

mutants and mitochondrial membranes form nets. Remark: is also called YJL112w, NET2, FIS2 or GAG3. Title: strong similarity to mitochondrial fission protein Mdv1 - *Saccharomyces cerevisiae*"
/citation=[77]
/citation=[78]
/codon-start=1
/protein-id="CAK42161.1"
/db-xref="GI:134081906"
/translation="MDKHRRRDESPGLSDIVEP
DGLLGITSRHIEAFGRKVTSTA
GHLMGPA PDSSTGGHYHTAMADIQREL RHPNTQR
KVFSLTQTTP TDLVRSKLSTTEIQ
SRAISSLPDELLANIPDDSSSYSLFQGFQASQDD
IEYRRRAHRRRSKSKLLKDGETR
GALPSAPSDLKKERDLSRRMELMGVRKNMCSSE
IHDIDNKIANLHNMKRIVLDRLAG
LEMEEADLEHELNEIENKLEDIQEEQAEVPPPP
ATPKSSEANDDSIVSEDPAMGASF
MSESIYQKIPSPKSVKQRSIILHEHFAPGSEIKE
MPAHSMDMTAIDFDYFPFGT MISAA
LDDTVRVVDLNVGRCVGFLEGNASVRCLQIEDN
IVATGSMASVVKLWDL SRARTTTR
DNRVTRREDDEESAQADDASMAHSSTTLED CYVY
SLDAHVEVTALHFKGDTLISGSA
DKTLRQWDLVKGRVCVQTL DVLWAAAQASTLGSET
TWRP SGRLPDASADFVGAVQCFDA
ALACGTADGMVRLWDLRSGQVHRS LVGHTGPITC
LQFDDVHLVTGSQDRSIRIIDLRT
GSIFDAYAYDKPITSMMEFDTKRIVAAAGENVVKV
YDKADGHHWD CGAGVGVDSDGPGP
ATVERVRLKDGFLVEGRKDGIVAAWTC"

exon	complement(208451..208726)	/locus-tag="An14g06000"
		/number=1
intron	complement(208727..208777)	/locus-tag="An14g06000"
		/number=1
exon	complement(208778..209568)	/locus-tag="An14g06000"
		/number=2
intron	complement(209569..209633)	/locus-tag="An14g06000"
		/number=2
exon	complement(209634..209834)	/locus-tag="An14g06000"
		/number=3
intron	complement(209835..209888)	/locus-tag="An14g06000"
		/number=3
exon	complement(209889..210489)	/locus-tag="An14g06000"
		/number=4
intron	complement(210490..210571)	/locus-tag="An14g06000"
		/number=4
exon	complement(210572..210658)	/locus-tag="An14g06000"
		/number=5
gene	<211445..>212528	/locus-tag="An14g06010"

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mRNA      join(<211445..211515, /locus-tag="An14g06010"
          211743..212394,
          212451..>212528)
CDS        join(211445..211515, /locus-tag="An14g06010"
          211743..212394,
          212451..212528)

          /EC-number="5.4.99.5"
          /inference="profile:COGS:COG1605"
          /inference="profile:PFAM:PF01817"
          /inference="similar to AA
          sequence:UniProtKB:AF133241.1"
          /note="unnamed protein product;
          Catalytic activity: chorismate
          mutases convert chorismate <=>
          prephenate. Function: aroC of A.
          nidulans is an allosterically
          regulated chorismate mutase acting
          at the first branch point of
          aromatic amino acid biosynthesis
          to generate prephenate. Induction:
          tryptophan acts as heterotropic
          activator of aroC from A.
          nidulans. Repression: tyrosine act
          as negative acting, heterotropic
          feedback-inhibitor of aroC from A.
          nidulans. Title: strong similarity
          to chorismate mutase aroC
          -Aspergillus nidulans cytoplasm"
          /citation=[60]
          /codon-start=1
          /protein-id="CAK42162.1"
          /db-xref="GI:134081907"
          /db-xref="GOA:A2R3Z4"
          /translation="MDTAIDLSDASKALDLANIR
          FQLIRLEDITITFHLIERAQFPLNK
          PIYLSGGVKIPGTDLSLLDYFLREQERLESVRVR
          YQSPDEYPPFFPDSLEEPILAPIKY
          PKILHDNDVNVNSTLQRYIEDILPAVCAQFGRE
          DRGEAQENYGSAATCDVHCLQALS
          RRIHFGKFVAEAKFQQETERFVKLIKANDRKGID
          DAITKPEVELKVLERLALKAKTYG
          TDPGFQEPENGPKINVDVAVMYKEYVIPLTKVVE
          VDYLMLQRLKGTQWE"
          /locus-tag="An14g06010"
          /number=1
          /locus-tag="An14g06010"
          /number=1
          /locus-tag="An14g06010"
          /number=2
          /locus-tag="An14g06010"
          /number=2
          /locus-tag="An14g06010"
          /number=3
          gene      complement(<212729..>21 /locus-tag="An14g06020"
          3754)
mRNA      complement(join(<212729 /locus-tag="An14g06020"
          ..213283,
          213342..213578,
          213671..>213754))
CDS        complement(join(212729. /locus-tag="An14g06020"
          .213283,213342..213578,
          213671..213754))

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/inference="similar to AA
sequence:PIR:T41474"
/note="unnamed protein product;
Similarity: the ORF shows
similarity to putative cdk
inhibitor p21 binding protein
TOK-1 of H. sapiens. Title: strong
similarity to hypothetical cdk
inhibitor p21 binding protein
SPCC613.08 -Schizosaccharomyces
pombe"
/codon-start=1
/protein-id="CAK42163.1"
/db-xref="GI:134081908"
/translation="MVKRKELKDNVEMSGTDPR
VDGDDSDDEMDMVNVDFEFDPQP
AVDFHGLKNLLRQLFDITDAQIFDMSALADLILSQ
PLLGSTVVKVDGNESDPYAFITVLN
LQEHKDKPVIKDLTAYLQRKANAVPTLAPLAQLL
SQTPIPPIGLILTERLINMPAEVV
PPMYTMLQEEIEWAIKDKEPYNFSHYLIVSKTYE
EVESKLDAAEESRPQKKKKAAGGE
KAERFLFHPDEVLERHAVCVGPVEYTHKAEGL
SDAKRAFQDLGIVTKGLILLEAS
KLDGAVKDMAEYFKP"
exon      complement(212729..2132 /locus-tag="An14g06020"
83)
intron    complement(213284..2133 /locus-tag="An14g06020"
41)
exon      complement(213342..2135 /locus-tag="An14g06020"
78)
intron    complement(213579..2136 /locus-tag="An14g06020"
70)
exon      complement(213671..2137 /locus-tag="An14g06020"
54)
gene      <214408..>214606 /locus-tag="An14g06030"
mRNA      join(<214408..>214444, /locus-tag="An14g06030"
214506..>214606)
CDS       join(214408..214444, /locus-tag="An14g06030"
214506..>214606)
/note="Remark: the predicted ORF
is only 45 amino acids long."
/codon-start=1
/product="hypothetical protein"
/protein-id="CAK42164.1"
/db-xref="GI:134081909"
/translation="MPFAQNGDAVTKADYQVEEG
IKYLREVKTTTLHPFVVKAPSVGSY T"
exon      214408..214444 /locus-tag="An14g06030"
intron    214445..214505 /locus-tag="An14g06030"
exon      214506..214606 /locus-tag="An14g06030"
gene      complement(<216128..>21 /locus-tag="An14g06040"
7084)
mRNA      complement(<216128..>21 /locus-tag="An14g06040"

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7084)
CDS complement(216128..2170 /locus-tag="An14g06040"
84)
/inference="profile:COGS:COG0599"
/inference="similar to AA
sequence:PIR:T39714"
/note="unnamed protein product;
Similarity: the predcited ORF is
96 amino acids longer at the
N-terminus than the hypothetical
protein SPBC17D11.03c of S.
pombe. Title: weak similarity to
hypothetical protein SPBC17D11.03c
- Schizosaccharomyces pombe"
/codon-start=1
/protein-id="CAK42165.1"
/db-xref="GI:134081910"
/translation="MARNPSRLLPSPRSLLQTTSS
KRQFGTGASILPLLSPPRYRPLRS
SLISSTPSSSPLAHRIFTATPLRTITTSNSAP
TKMTTIDPKYAQLFQSLESQFQT
TTLPHDKWYILAISTLVANPDPERADQLYLYLTS
KPEYSTPSSRQDLIRRIREALIKS
VIIIVGVCKPIEAILAISKEAPEDKDYFTFTRENW
QCDEANHERGVAVLEKLYARNTSG
TLDLFAAHKDFAWLSKEITYGLFLSDRGVLDLDDLD
TQLVVLPAIMSNLKIETHWHIRG
TRRLGVSLEDVRLCEGVKHHVAGFYGRVLDKVPSS
VEEVEGDV"
exon complement(216128..2170 /locus-tag="An14g06040"
84)
gene <217593..>218104 /number=1
mRNA join(<217593..217931, /locus-tag="An14g06050"
218003..>218104) /locus-tag="An14g06050"
CDS join(217593..217931, /locus-tag="An14g06050"
218003..218104)
/note="unnamed protein product;
Title: weak similarity to
hypothetical protein B10H18.060 -
Neurospora crassa"
/codon-start=1
/protein-id="CAK42166.1"
/db-xref="GI:134081911"
/translation="MSSSGAGQSSVGSRAIYEAG
DQRNVQPQSEINEQNRYAEGQKNSH
KNLDSMPSPSSLLPSNHSQDIVLTNTKTEDQRSI
GNKLASQERKPESDHHNFDQNP
AELSKQDPTKPAKVHGNPESKGAIDAEQAED
QRLREKGIKK"
exon 217593..217931 /locus-tag="An14g06050"
/number=1
intron 217932..218002 /locus-tag="An14g06050"
/number=1
exon 218003..218104 /locus-tag="An14g06050"
/number=2
gene complement(<218542..>21 /locus-tag="An14g06060"
9708)
mRNA complement(<218542..>21 /locus-tag="An14g06060"
9708)
CDS complement(218542..2197 /locus-tag="An14g06060"
08)

/inference="similar to AA
 sequence:UniProtKB:SC05211.1"
 /note="unnamed protein product;
 Function: TTP1 of *S. cerevisiae* is
 involved in the transfer of
 mannose residues to the mannans of
 glycoproteins during maturation in
 the Golgi. Function: the correct
 mannosylation of proteins by TTP1
 of *S. cerevisiae* is essential for
 growth and morphogenesis. Golgi
 Phenotype: the N-linked sugar
 residues in the *S. cerevisiae* TTP1
 null mutant lack the main
 alpha-1,2-linked branches of the
 mannan. Remark: TTP1 of *S.*
cerevisiae is also called mnn2 or
 YBR015C. Title: strong similarity
 to alpha-1,2-mannosyltransferase
 Ttp1 - *Saccharomyces cerevisiae*"
 /citation=[43]
 /citation=[56]
 /citation=[57]
 /codon-start=1
 /protein-id="CAK42167.1"
 /db-xref="GI:134081912"
 /translation="MEESHAGYIEECRKAERLRP
 VHTPGTRGIVSTAGASYFPVFLSS
 LRMLRLRLGSTLPVEVYMKDKSEYKQICDDILPD
 LGARCLVLSDIVGKGAIEHYQLKI
 FAVLFSSFEFVIWMDADCFPLHKPEVLLESEPT
 SKGLVTWPDFWISSAPLYFTISR
 QEMPALSERASSEAGVFLVSKKTHQMTLLLAAYY
 NYYGPSHYFRLLSQGAPGEGDKET
 FLHAASAVGEPFYAVSERVQAVGHKTPGGIAGSA
 MVQTDPAEDYALTSAGKWRVQDES
 VAKAPRAFFIHANYPKFNPGEKVFGMKWETIPTL
 RPDGTDGRAWLVAESTVQRFYDV
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221941	cgaccgcgct	gcgccatttt	gctcccagct	cttggacagc	gcccgcgaat	gcgcggggtg
222001	caagacagcg	ttgacatggg	gcgtaggagt	tgccagctcg	ggaaagcttc	gaggtattgc
222061	ctctccccgt	agccgggacg	agcctcggtg	cgcacccccg	aaagctcccc	gtgcgacagg
222121	tcacagagca	gtgtccaaat	cgcaaccggc	tcttgacaca	gcccgcagaa	aacgcagcat
222181	tcattgataa	cagcgttcat	cagccgcggg	gcttacagag	catgggtctg	tctcgattcc
222241	acctacttca	caacgcgcgt	tgtgctcacc	ggagtactac	actgtggatt	cccatgttaa
222301	gccgaatcac	ctataactct	attcttcacg	tgcgacaaag	accgattctt	tgaacaataa
222361	ccatgcccca	ttggtcgcaa	accocgatcc	atcaagggcc	tggtatgggt	taaacacagc
222421	accggtacgc	atacagtgct	cgtggccagc	cctgactccg	gaacagaaag	ataagtgttc
222481	ggatgagcaa	ctcagaagaa	cctcttataa	cgaagtttca	ccacgtatga	gtccttgcca
222541	gcgcgcatac	ttatctcagc	agctgctggc	gcgttccgtg	ggacgtacac	ctcgacttgc
222601	atacctaatt	agttatttat	cgaagatcat	tgtcccgatg	attgtggcat	ttgatattgc
222661	aaccaatcct	tttcgaacat	atatcctcgc	actggcgcag	gagagcacat	gcctcaaga
222721	agccatacgc	acgcttggcaa	gctgcaatct	cgcacagcga	cgcgcacagc	cgcagaggtc
222781	gacggagcga	actttgcggg	ggcgccctgc	gtccatggcc	catcaagcct	tgaccgacgg
222841	agcattacag	gaccggacgc	gtatctttat	gcctgaagat	tatggccagg	aagagcagta
222901	tcactgaggg	agtcgggtct	ccgccttgaa	tccggaaatt	gcgcactcac	atcagaggtc
222961	ttcagactcc	gtccttggca	ccttactcat	cctctgtcta	ttccacgggt	gtgatactgg
223021	gttggtctca	ttcaagacc	agtttgcggg	ggtgacaaaa	ttgttggtta	ttcgactgtc
223081	caactcacct	tgcattgtcg	atgaactgaa	gtggtttgtt	cgcatgttca	catggattga
223141	cacgatgacc	gccaccacca	atgaccgcga	gttcacagct	cgcggtgctt	ctcggtatat
223201	caccgcgcgc	tcagatggcg	aatggggact	ggaaaaattc	gcgggctgtg	atgcgcgact
223261	tttcagaatt	gtgcgcagc	taggttcggt	gaacctttct	agtcaaaact	aagaagttcc
223321	cacatctaac	ccaccagaca	tccatatacc	atccactact	ctccccccct	cgatggcggt
223381	cttccactgc	aaccttccag	ccacctctgc	cggtcttttt	gcattttacct	tggccgcgct
223441	gcgcctctct	ggtgatcgcg	acagaggaca	gctgccgcgc	cggttctggg	tgcaatggtg
223501	ttctctccga	cagaagcttg	agtcctggcg	atttgttccc	caccaatcgc	agtcacagtc
223561	acctctcttt	actctccagc	acgcctacat	ctcgccacct	tcactgcgcg	cagaccagcc
223621	gggtgctcga	gctcacaaat	tcaaggacgt	catcacacat	tcgtgactat	tccgtcatgc
223681	ggcgactctg	tacagcgagc	gactcgccca	tccagacctc	ccgtccgcat	acctcgatat
223741	tcaaaactat	gtgcaacaca	taatgagtca	cattatgact	gttcaaatct	agccgatatt
223801	ctctgtgccca	ctattcatca	cgggttcgga	gtgcgtgcgt	ggcgtatcat	cgcgcattat
223861	cgcccaacgc	tgcaaaagat	tatccaggga	ctctgggttc	ttcaacaaac	tctcatgctt
223921	gcagctcctg	gagaaagatc	gggcagagaa	ccctgcgctg	gatgtgatcc	ctgttgcttc
223981	atccccgtgat	tccggtctgc	agggcagcgc	cagcgggtgc	gtgacggagg	ttacattttc
224041	cccgccctgga	agctgggctc	cgtcccagca	tgagggtctc	atgtctccga	cactgccttc
224101	tgctctctcg	aagcagggat	tccgcttgca	cgaaggcgat	caaaccaaac	gcgcggaggg
224161	cgagtatatg	actgtatgac	gtgacctgac	ggatacgtgc	atcaaaacga	cgagtccagc
224221	atgaatttgcg	agaccaaatt	ataatataga	ggatatcatat	tagcgaataa	taatgaacat
224281	aatgcaacat	ttccccacta	cgtacacagt	actgtgtgcc	ctcagtatct	gtctatggca
224341	acctgaacct	tccgggccaca	acaggccccc	actatcgga	ctctcgcatc	agatccgttc
224401	ccacttccca	cacaactccg	tcgatacgtg	ccatcacgac	agtaacctac	tgcgtaaaaa
224461	tctcgtataa	cctactgtca	tctgtcgaaa	ctccatcgat	gatcactcta	ctccacttgc
224521	ttcctctagc	aacctgcttc	accagcccac	ccaaacaaac	cacaaaaagt	gcccgcacgg
224581	gcattctccc	agcgcacgta	cgtcggaaaa	tttgtgttgc	aggtgagttg	agtttccggt
224641	ctcgtgtgta	gtgctcattt	tgtgggtgtt	ggactctgag	aggggttcca	ccatcaactt
224701	agatagtact	gtgcgcgtgt	gggtgataga	tgagtgggta	agtaatttgc	taactcttgg
224761	agagaagggg	tcttgttacc	tttgtttctt	gaattactgg	tttgttatgt	cgaggggggg
224821	gtctactgtg	ctgcgccagt	atactatcta	tggctacata	gggaactaac	actacataga
224881	gtagttagca	tgtagttaa	gcacagtagt	ataccactat	tatagtaata	gtatggcagc
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225001	cccaataata	gtgaacgctc	atgcacatgt	ccatgctctc	tctctacatt	atttaactaac
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 226501 tta

L5 ANSWER 26 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AE014133 GenBank (R)
 GenBank ACC. NO. (GBN): AE014133 AE014853-AE015037
 GenBank VERSION (VER): AE014133.1 GI:24378526
 SEQUENCE LENGTH (SQL): 2030921
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 24 Jan 2006
 DEFINITION (DEF): Streptococcus mutans UA159, complete genome.
 SOURCE: Streptococcus mutans UA159
 ORGANISM (ORGN): Streptococcus mutans UA159
 Bacteria; Firmicutes; Lactobacillales;
 Streptococcaceae; Streptococcus

COMMENT:

On or before Jan 18, 2006 this sequence version replaced
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gi:24377983, gi:24377998, gi:24378012, gi:24378027, gi:24378041,
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gi:24378472, gi:24378487, gi:24378500, gi:24378511, gi:24378520.

REFERENCE: 1 (bases 1 to 2030921)

AUTHOR (AU): Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;
Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;
Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najjar,F.;
Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.

TITLE (TI): Genome sequence of *Streptococcus mutans* UA159, a
cariogenic dental pathogen

JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (22), 14434-14439
(2002)

OTHER SOURCE (OS): CA 137:364100

REFERENCE: 2 (bases 1 to 2030921)

AUTHOR (AU): Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;
Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;
Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najjar,F.;
Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (09-JUL-2002) Department of Microbiology and
Immunology, University of Oklahoma Health Sciences
Center, 940 SL Young Blvd., Oklahoma City, OK 73104,
USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2030921	/organism="Streptococcus mutans UA159" /mol-type="genomic DNA" /strain="UA159" /db-xref="taxon:210007"

L5 ANSWER 27 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): BX571856 GenBank (R)

GenBank ACC. NO. (GBN): BX571856

GenBank VERSION (VER): BX571856.1 GI:49240382

CAS REGISTRY NO. (RN): 726687-34-9

SEQUENCE LENGTH (SQL): 2902619

MOLECULE TYPE (CI): DNA; circular

DIVISION CODE (CI): Bacteria

DATE (DATE): 7 Oct 2006

DEFINITION (DEF): *Staphylococcus aureus* subsp. *aureus* strain MRSA252,
complete genome.

KEYWORDS (ST): complete genome

SOURCE: *Staphylococcus aureus* subsp. *aureus* MRSA252

ORGANISM (ORGN): *Staphylococcus aureus* subsp. *aureus* MRSA252

REFERENCE: Bacteria; Firmicutes; Bacillales; Staphylococcus
1 (bases 1 to 2902619)
AUTHOR (AU): Holden,M.T.; Feil,E.J.; Lindsay,J.A.; Peacock,S.J.;
Day,N.P.; Enright,M.C.; Foster,T.J.; Moore,C.E.;
Hurst,L.; Atkin,R.; Barron,A.; Bason,N.; Bentley,S.D.;
Chillingworth,C.; Chillingworth,T.; Churcher,C.;
Clark,L.; Corton,C.; Cronin,A.; Doggett,J.; Dowd,L.;
Feltwell,T.; Hance,Z.; Harris,B.; Hauser,H.;
Holroyd,S.; Jagels,K.; James,K.D.; Lennard,N.; Line,A.;
Mayes,R.; Moule,S.; Mungall,K.; Ormond,D.; Quail,M.A.;
Rabinowitsch,E.; Rutherford,K.; Sanders,M.; Sharp,S.;
Simmonds,M.; Stevens,K.; Whitehead,S.; Barrell,B.G.;
Spratt,B.G.; Parkhill,J.
TITLE (TI): Complete genomes of two clinical Staphylococcus aureus
strains: evidence for the rapid evolution of virulence
and drug resistance
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 101 (26), 9786-9791
(2004)
OTHER SOURCE (OS): CA 141:152000
REFERENCE: 2 (bases 1 to 2902619)
AUTHOR (AU): Holden,M.T.G.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (23-JUN-2004) Submitted on behalf of the
Pathogen Sequencing Unit, Sanger Institute, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 1SA,
E-mail: mh3@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2902619	/organism="Staphylococcus aureus subsp. aureus MRSA252" /mol-type="genomic DNA" /strain="MRSA252" /sub-species="aureus" /db-xref="taxon:282458"

=> d 15 20

L5 ANSWER 20 OF 27 USPATFULL on STN
AN 2003:71519 USPATFULL
TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF
Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF
Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF
PI US 20030049804 A1 20030313
AI US 2000-746660 A1 20001222 (9)
RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
2000, PENDING
PRAI DE 1999-19931420 19990708
US 1999-141031P 19990625 (60)
US 1999-142101P 19990702 (60)
US 1999-148613P 19990812 (60)
US 2000-187970P 20000309 (60)

DT Utility
FS APPLICATION
LN.CNT 15004
INCL INCLM: 435/115.000
INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200
NCL NCLM: 435/115.000
NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200
IC [7]
ICM C12P013-08
ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21
IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
C07H0021-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];
C12N0001-21 [ICS,7]
IPCR C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];
C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];
C12N0009-90 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 21

L5 ANSWER 21 OF 27 USPATFULL on STN
AN 2003:95966 USPATFULL
TI Polynucleotides, materials incorporating them, and methods for using
them
IN Glenn, Matthew, Auckland, NEW ZEALAND
Havukkala, Ilkka J., Auckland, NEW ZEALAND
Blokberg, Leonard N., Auckland, NEW ZEALAND
Lubbers, Mark W., Palmerston North, NEW ZEALAND
Dekker, James, Palmerston North, NEW ZEALAND
Christensson, Anna C., Lund, SWEDEN
Holland, Ross, Palmerston North, NEW ZEALAND
O'Toole, Paul W., Palmerston North, NEW ZEALAND
Reid, Julian R., Palmerston North, NEW ZEALAND
Coolbear, Timothy, Palmerston North, NEW ZEALAND
PA Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.
corporation)
Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.
corporation)
PI US 6544772 B1 20030408
AI US 2000-634238 20000808 (9)
DT Utility
FS GRANTED
LN.CNT 2015
INCL INCLM: 435/252.300
INCLS: 435/320.100; 536/023.700
NCL NCLM: 435/252.300
NCLS: 435/320.100; 536/023.700
IC [7]
ICM C12N001-21
ICS C12N015-63; C12N015-31
IPCI C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]
IPCR A23C0019-00 [I,C*]; A23C0019-032 [I,A]; C07K0014-195 [I,C*];
C07K0014-335 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
C12N0015-31 [I,C*]; C12N0015-31 [I,A]
EXF 435/252.3; 435/320.1; 536/23.7
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 22

L5 ANSWER 22 OF 27 BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS on STN
 AN 1999-00562 BIOTECHDS
 TI Use of lactic and propionic acid bacteria;
 to bind mycotoxin to prevent their absorption or to purify
 contaminated food or feedstuff
 AU El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J
 PA Roy.Melbourne-Inst.Technol.
 LO Melbourne, Victoria, Australia.
 PI WO 9834503 13 Aug 1998
 AI WO 1998-AU63 6 Feb 1998
 PRAI AU 1997-5005 7 Feb 1997
 DT Patent
 LA English
 OS WPI: 1998-557001 [49]

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(FILE 'HOME' ENTERED AT 13:55:21 ON 07 JUL 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONO2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:55:47 ON 07 JUL 2008
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 SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND? AND CD4+ CELLS

0* FILE ADISCTI
 SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND?

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 0* FILE AQUALINE
 0* FILE BIOENG
 1* FILE BIOTECHABS
 1* FILE BIOTECHDS
 0* FILE BIOTECHNO
 2 FILE CAPLUS
 0* FILE CEABA-VTB
 0* FILE CIN
 0* FILE EMBIOBASE
 0* FILE FOMAD
 0* FILE FOREGE
 2* FILE FROSTI
 0* FILE FSTA
 5 FILE GENBANK
 1 FILE IFIPAT
 0* FILE KOSMET
 0* FILE NTIS
 0* FILE NUTRACEUT
 1* FILE PASCAL
 0* FILE PHARMAML
 1 FILE SCISEARCH
 1 FILE TOXCENTER
 21 FILE USPATFULL
 3 FILE USPAT2
 0* FILE WATER
 2 FILE WPIDS
 2 FILE WPINDEX

L1 QUE LACTOBACILLUS REUTERI AND TOXIN(P) BIND?

FILE 'BIOTECHDS, CAPLUS, FROSTI, GENBANK, IFIPAT, PASCAL, SCISEARCH,
TOXCENTER, USPATFULL, USPAT2' ENTERED AT 13:59:37 ON 07 JUL 2008

L2 38 S L1
L3 34 DUP REM L2 (4 DUPLICATES REMOVED)
L4 27 S L3 AND (TABLET OR FOOD OR DIETARY SUPPLEMENT OR CONFECTIONERY
L5 27 DUP REM L4 (0 DUPLICATES REMOVED)

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=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

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INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 17:02:31 ON 29 MAR 2009

68 FILES IN THE FILE LIST IN STNINDEX

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=> s Lactobacillus reuteri and toxi? and CD+4(p)lymphocyte? and cultur?

0* FILE ADISNEWS

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0* FILE BIOENG


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0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
0* FILE CEABA-VTB
0* FILE CIN
21 FILES SEARCHED...
0* FILE FOMAD
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0* FILE FROSTI
0* FILE FSTA
0* FILE KOSMET
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0* FILE NTIS
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61 FILES SEARCHED...
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L1 QUE LACTOBACILLUS REUTERI AND TOXI? AND CD+4(P) LYMPHOCYTE? AND CULTUR?

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